

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wood, John N.
Akopian, Armen N.
- (ii) TITLE OF INVENTION: Ion Channel
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: ZENECA Pharmaceuticals
 - (B) STREET: 1800 Concord Pike, P.O. Box 15437
 - (C) CITY: Wilmington
 - (D) STATE: Delaware
 - (E) COUNTRY: USA
 - (F) ZIP: 19850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/669,656
 - (B) FILING DATE: 24-JUN-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hohenschutz, Liza D.
 - (B) REGISTRATION NUMBER: 33,712
 - (C) REFERENCE/DOCKET NUMBER: PHM.70086
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (302) 886-7466

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 204..6077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAGCTTGCTT CTGCTAATGC TACCCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG	60
TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTTC	120
AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAAA GAGTGTAAT	180

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TCTTCCCCAA	GAAGAATGAG	AAG	ATG	GAG	CTC	CCC	TTT	GCG	TCC	GTG	GGA						230
			Met	Glu	Leu	Pro	Phe	Ala	Ser	Val	Gly						
			1				5										
ACT	ACC	AAT	TTC	AGA	CGG	TTC	ACT	CCA	GAG	TCA	CTG	GCA	GAG	ATC	GAG		278
Thr	Thr	Asn	Phe	Arg	Arg	Phe	Thr	Pro	Glu	Ser	Leu	Ala	Glu	Ile	Glu		
10					15				20						25		
AAG	CAG	ATT	GCT	GCT	CAC	CGC	GCA	GCC	AAG	AAG	GCC	AGA	ACC	AAG	CAC		326
Lys	Gln	Ile	Ala	Ala	His	Arg	Ala	Ala	Lys	Lys	Ala	Arg	Thr	Lys	His		
			30						35					40			
AGA	GGA	CAG	GAG	GAC	AAG	GGC	GAG	AAG	CCC	AGG	CCT	CAG	CTG	GAC	TTG		374
Arg	Gly	Gln	Glu	Asp	Lys	Gly	Glu	Lys	Pro	Arg	Pro	Gln	Leu	Asp	Leu		
			45					50					55				
AAA	GAC	TGT	AAC	CAG	CTG	CCC	AAG	TTC	TAT	GGT	GAG	CTC	CCA	GCA	GAA		422
Lys	Asp	Cys	Asn	Gln	Leu	Pro	Lys	Phe	Tyr	Gly	Glu	Leu	Pro	Ala	Glu		
		60					65					70					
CTG	GTC	GGG	GAG	CCC	CTG	GAG	GAC	CTA	GAC	CCT	TTC	TAC	AGC	ACA	CAC		470
Leu	Val	Gly	Glu	Pro	Leu	Glu	Asp	Leu	Asp	Pro	Phe	Tyr	Ser	Thr	His		
	75					80					85						
CGG	ACA	TTC	ATG	GTG	TTG	AAT	AAA	AGC	AGG	ACC	ATT	TCC	AGA	TTC	AGT		518
Arg	Thr	Phe	Met	Val	Leu	Asn	Lys	Ser	Arg	Thr	Ile	Ser	Arg	Phe	Ser		
90					95				100						105		
GCC	ACT	TGG	GCC	CTG	TGG	CTC	TTC	AGT	CCC	TTC	AAC	CTG	ATC	AGA	AGA		566
Ala	Thr	Trp	Ala	Leu	Trp	Leu	Phe	Ser	Pro	Phe	Asn	Leu	Ile	Arg	Arg		
				110					115					120			
ACA	GCC	ATC	AAA	GTG	TCT	GTC	CAT	TCC	TGG	TTC	TCC	ATA	TTC	ATC	ACC		614
Thr	Ala	Ile	Lys	Val	Ser	Val	His	Ser	Trp	Phe	Ser	Ile	Phe	Ile	Thr		
			125					130					135				
ATC	ACT	ATT	TTG	GTC	AAC	TGC	GTG	TGC	ATG	ACC	CGA	ACT	GAT	CTT	CCA		662
Ile	Thr	Ile	Leu	Val	Asn	Cys	Val	Cys	Met	Thr	Arg	Thr	Asp	Leu	Pro		
	140					145						150					
GAG	AAA	GTC	GAG	TAC	GTC	TTC	ACT	GTC	ATT	TAC	ACC	TTC	GAG	GCT	CTG		710
Glu	Lys	Val	Glu	Tyr	Val	Phe	Thr	Val	Ile	Tyr	Thr	Phe	Glu	Ala	Leu		
	155					160					165						
ATT	AAG	ATA	CTG	GCA	AGA	GGG	TTT	TGT	CTA	AAT	GAG	TTC	ACT	TAT	CTT		758
Ile	Lys	Ile	Leu	Ala	Arg	Gly	Phe	Cys	Leu	Asn	Glu	Phe	Thr	Tyr	Leu		
170					175				180						185		
CGA	GAT	CCG	TGG	AAC	TGG	CTG	GAC	TTC	AGT	GTC	ATT	ACC	TTG	GCG	TAT		806
Arg	Asp	Pro	Trp	Asn	Trp	Leu	Asp	Phe	Ser	Val	Ile	Thr	Leu	Ala	Tyr		
				190					195					200			
GTG	GGT	GCA	GCG	ATA	GAC	CTC	CGA	GGA	ATC	TCA	GGC	CTG	CGG	ACA	TTC		854
Val	Gly	Ala	Ala	Ile	Asp	Leu	Arg	Gly	Ile	Ser	Gly	Leu	Arg	Thr	Phe		
			205					210					215				
CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG		902
Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys		
		220				225						230					
GTC	ATC	GTG	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG		950
Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val		
	235					240					245						

ACT Thr 250	ATC Ile	CTC Leu	ACA Thr	GTC Val	TTC Phe 255	TGC Cys	CTG Leu	AGC Ser	GTC Val	TTC Phe 260	GCC Ala	TTG Leu	GTG Val	GGC Gly	CTG Leu 265	998
CAG Gln	CTC Leu	TTT Phe	AAG Lys	GGG Gly 270	AAC Asn	CTT Leu	AAG Lys	AAC Asn	AAA Lys 275	TGC Cys	ATC Ile	AGG Arg	AAC Asn	GGA Gly 280	ACA Thr	1046
GAT Asp	CCC Pro	CAC His	AAG Lys 285	GCT Ala	GAC Asp	AAC Asn	CTC Leu	TCA Ser 290	TCT Ser	GAA Glu	ATG Met	GCA Ala	GAA Glu 295	TAC Tyr	GTC Val	1094
TCC Ser	ATC Ile	AAG Lys 300	CCT Pro	GGT Gly	ACT Thr	ACG Thr	GAT Asp 305	CCC Pro	TTA Leu	CTG Leu	TGC Cys	GGC Gly 310	AAT Asn	GGG Gly	TCT Ser	1142
GAT Asp 315	GCT Ala	GGT Gly	CAC His	TGC Cys	CCT Pro	GGA Gly 320	GGC Gly	TAT Tyr	GTC Val	TGC Cys	CTG Leu 325	AAA Lys	ACT Thr	CCT Pro	GAC Asp	1190
AAC Asn 330	CCG Pro	GAT Asp	TTT Phe	AAC Asn	TAC Tyr 335	ACC Thr	AGC Ser	TTT Phe	GAT Asp	TCC Ser 340	TTT Phe	GCG Ala	TGG Trp	GCA Ala	TTC Phe 345	1238
CTC Leu	TCA Ser	CTG Leu	TTC Phe	CGC Arg 350	CTC Leu	ATG Met	ACG Thr	CAG Gln	GAC Asp 355	TCC Ser	TGG Trp	GAG Glu	CGC Arg	CTG Leu 360	TAC Tyr	1286
CAG Gln	CAG Gln	ACA Thr 365	CTC Leu	CGG Arg	GCT Ala	TCT Ser	GGG Gly 370	AAA Lys 370	ATG Met	TAC Tyr	ATG Met	GTC Val	TTT Phe 375	TTC Phe	GTG Val	1334
CTG Leu	GTT Val 380	ATT Ile	TTC Phe	CTT Leu	GGA Gly	TCG Ser	TTC Phe 385	TAC Tyr	CTG Leu	GTC Val	AAT Asn 390	TTG Leu	ATC Ile	TTG Leu	GCC Ala	1382
GTG Val 395	GTC Val	ACC Thr	ATG Met	GCG Ala	TAT Tyr 400	GAA Glu	GAG Glu	CAG Gln	AGC Ser	CAG Gln	GCA Ala 405	ACA Thr	ATT Ile	GCA Ala	GAA Glu	1430
ATC Ile 410	GAA Glu	GCC Ala	AAG Lys	GAA Glu	AAA Lys 415	AAG Lys	TTC Phe	CAG Gln	GAA Glu	GCC Ala 420	CTT Leu	GAG Glu	GTG Val	CTG Leu	CAG Gln 425	1478
AAG Lys	GAA Glu	CAG Gln	GAG Glu	GTG Val 430	CTG Leu	GCA Ala	GCC Ala	CTG Leu	GGG Gly 435	ATT Ile	GAC Asp	ACG Thr	ACC Thr	TCG Ser 440	CTC Leu	1526
CAG Gln	TCC Ser	CAC His 445	AGT Ser	GGA Gly	TCA Ser	CCC Pro	TTA Leu	GCC Ala 450	TCC Ser	AAA Lys	AAC Asn	GCC Ala	AAT Asn 455	GAG Glu	AGA Arg	1574
AGA Arg	CCC Pro	AGG Arg 460	GTG Val	AAA Lys	TCA Ser	AGG Arg	GTG Val 465	TCA Ser	GAG Glu	GGC Gly	TCC Ser	ACG Thr 470	GAT Asp	GAC Asp	AAC Asn	1622
AGG Arg 475	TCA Ser	CCC Pro	CAA Gln	TCT Ser	GAC Asp	CCT Pro 480	TAC Tyr	AAC Asn	CAG Gln	CGC Arg	AGG Arg 485	ATG Met	TCT Ser	TTC Phe	CTA Leu	1670
GGC Gly 490	CTG Leu	TCT Ser	TCA Ser	GGA Gly	AGA Arg 495	CGC Arg	AGG Arg	GCT Ala	AGC Ser	CAC His 500	GGC Gly	AGT Ser	GTG Val	TTC Phe	CAC His 505	1718

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TTC	CGA	GCG	CCC	AGC	CAA	GAC	ATC	TCA	TTT	CCT	GAC	GGG	ATC	ACC	CCT	1766
Phe	Arg	Ala	Pro	Ser	Gln	Asp	Ile	Ser	Phe	Pro	Asp	Gly	Ile	Thr	Pro	
				510					515					520		
GAT	GAT	GGG	GTC	TTT	CAC	GGA	GAC	CAG	GAA	AGC	CGT	CGA	GGT	TCC	ATA	1814
Asp	Asp	Gly	Val	Phe	His	Gly	Asp	Gln	Glu	Ser	Arg	Arg	Gly	Ser	Ile	
			525					530					535			
TTG	CTG	GGC	AGG	GGT	GCT	GGG	CAG	ACA	GGT	CCA	CTC	CCC	AGG	AGC	CCA	1862
Leu	Leu	Gly	Arg	Gly	Ala	Gly	Gln	Thr	Gly	Pro	Leu	Pro	Arg	Ser	Pro	
		540					545					550				
CTG	CCT	CAG	TCC	CCC	AAC	CCT	GGC	CGT	AGA	CAT	GGA	GAA	GAG	GGA	CAG	1910
Leu	Pro	Gln	Ser	Pro	Asn	Pro	Gly	Arg	Arg	His	Gly	Glu	Glu	Gly	Gln	
	555					560					565					
CTC	GGA	GTG	CCC	ACT	GGT	GAG	CTT	ACC	GCT	GGA	GCG	CCT	GAA	GGC	CCG	1958
Leu	Gly	Val	Pro	Thr	Gly	Glu	Leu	Thr	Ala	Gly	Ala	Pro	Glu	Gly	Pro	
570					575					580					585	
GCA	CTG	CAC	ACT	ACA	GGG	CAG	AAG	AGC	TTC	CTG	TCT	GCG	GGC	TAC	TTG	2006
Ala	Leu	His	Thr	Thr	Gly	Gln	Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	
				590					595					600		
AAC	GAA	CCT	TTC	CGA	GCA	CAG	AGG	GCC	ATG	AGC	GTT	GTC	AGT	ATC	ATG	2054
Asn	Glu	Pro	Phe	Arg	Ala	Gln	Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	
			605					610					615			
ACT	TCT	GTC	ATT	GAG	GAG	CTT	GAA	GAG	TCT	AAG	CTG	AAG	TGC	CCA	CCC	2102
Thr	Ser	Val	Ile	Glu	Glu	Leu	Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	
		620					625					630				
TGC	TTG	ATC	AGC	TTC	GCT	CAG	AAG	TAT	CTG	ATC	TGG	GAG	TGC	TGC	CCC	2150
Cys	Leu	Ile	Ser	Phe	Ala	Gln	Lys	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	
	635					640					645					
AAG	TGG	AGG	AAG	TTC	AAG	ATG	GCG	CTG	TTC	GAG	CTG	GTG	ACT	GAC	CCC	2198
Lys	Trp	Arg	Lys	Phe	Lys	Met	Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	
650					655					660					665	
TTC	GCA	GAG	CTT	ACC	ATC	ACC	CTC	TGC	ATC	GTG	GTG	AAC	ACC	GTC	TTC	2246
Phe	Ala	Glu	Leu	Thr	Ile	Thr	Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	
				670					675					680		
ATG	GCC	ATG	GAG	CAC	TAC	CCC	ATG	ACC	GAT	GCC	TTC	GAT	GCC	ATG	CTT	2294
Met	Ala	Met	Glu	His	Tyr	Pro	Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	
			685					690					695			
CAA	GCC	GGC	AAC	ATT	GTC	TTC	ACC	GTG	TTT	TTC	ACA	ATG	GAG	ATG	GCC	2342
Gln	Ala	Gly	Asn	Ile	Val	Phe	Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	
		700					705					710				
TTC	AAG	ATC	ATT	GCC	TTC	GAC	CCC	TAC	TAT	TAC	TTC	CAG	AAG	AAG	TGG	2390
Phe	Lys	Ile	Ile	Ala	Phe	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	
	715					720					725					
AAT	ATC	TTC	GAC	TGT	GTC	ATC	GTC	ACC	GTG	AGC	CTT	CTG	GAG	CTG	AGT	2438
Asn	Ile	Phe	Asp	Cys	Val	Ile	Val	Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	
730					735					740					745	
GCA	TCC	AAG	AAG	GGC	AGC	CTG	TCT	GTG	CTC	CGT	ACC	TTA	CGC	TTG	CTG	2486
Ala	Ser	Lys	Lys	Gly	Ser	Leu	Ser	Val	Leu	Arg	Thr	Leu	Arg	Leu	Leu	
				750					755					760		

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CGG	GTC	TTC	AAG	CTG	GCC	AAG	TCC	TGG	CCC	ACC	CTG	AAC	ACC	CTC	ATC	2534
Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	Thr	Leu	Ile	
			765					770					775			
AAG	ATC	ATC	GGG	AAC	TCA	GTG	GGG	GCC	CTG	GGC	AAC	CTG	ACC	TTT	ATC	2582
Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	Asn	Leu	Thr	Phe	Ile	
			780				785					790				
CTG	GCC	ATC	ATC	GTC	TTC	ATC	TTC	GCC	CTG	GTC	GGA	AAG	CAG	CTT	CTC	2630
Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Leu	Val	Gly	Lys	Gln	Leu	Leu	
	795					800					805					
TCA	GAG	GAC	TAC	GGG	TGC	CGC	AAG	GAC	GGC	GTC	TCC	GTG	TGG	AAC	GGC	2678
Ser	Glu	Asp	Tyr	Gly	Cys	Arg	Lys	Asp	Gly	Val	Ser	Val	Trp	Asn	Gly	
810					815					820					825	
GAG	AAG	CTC	CGC	TGG	CAC	ATG	TGT	GAC	TTC	TTC	CAT	TCC	TTC	CTG	GTC	2726
Glu	Lys	Leu	Arg	Trp	His	Met	Cys	Asp	Phe	Phe	His	Ser	Phe	Leu	Val	
				830					835					840		
GTC	TTC	CGA	ATC	CTC	TGC	GGG	GAG	TGG	ATC	GAG	AAC	ATG	TGG	GTC	TGC	2774
Val	Phe	Arg	Ile	Leu	Cys	Gly	Glu	Trp	Ile	Glu	Asn	Met	Trp	Val	Cys	
			845					850					855			
ATG	GAG	GTC	AGC	CAG	AAA	TCC	ATC	TGC	CTC	ATC	CTC	TTC	TTG	ACT	GTG	2822
Met	Glu	Val	Ser	Gln	Lys	Ser	Ile	Cys	Leu	Ile	Leu	Phe	Leu	Thr	Val	
			860				865					870				
ATG	GTG	CTG	GGC	AAC	CTA	GTG	GTG	CTC	AAC	CTT	TTC	ATC	GCT	TTA	CTG	2870
Met	Val	Leu	Gly	Asn	Leu	Val	Val	Leu	Asn	Leu	Phe	Ile	Ala	Leu	Leu	
			875			880					885					
CTG	AAC	TCC	TTC	AGC	GCG	GAC	AAC	CTC	ACG	GCT	CCA	GAG	GAT	GAC	GGG	2918
Leu	Asn	Ser	Phe	Ser	Ala	Asp	Asn	Leu	Thr	Ala	Pro	Glu	Asp	Asp	Gly	
890					895				900						905	
GAG	GTG	AAC	AAC	TTG	CAG	TTA	GCA	CTG	GCC	AGG	ATC	CAG	GTA	CTT	GGC	2966
Glu	Val	Asn	Asn	Leu	Gln	Leu	Ala	Leu	Ala	Arg	Ile	Gln	Val	Leu	Gly	
				910				915					920			
CAT	CGG	GCC	AGC	AGG	GCC	AGC	GCC	AGT	TAC	ATC	AGC	AGC	CAC	TGC	CGA	3014
His	Arg	Ala	Ser	Arg	Ala	Ser	Ala	Ser	Tyr	Ile	Ser	Ser	His	Cys	Arg	
			925					930					935			
TTC	CAC	TGG	CCC	AAG	GTG	GAG	ACC	CAG	CTG	GGC	ATG	AAG	CCC	CCA	CTC	3062
Phe	His	Trp	Pro	Lys	Val	Glu	Thr	Gln	Leu	Gly	Met	Lys	Pro	Pro	Leu	
			940				945					950				
ACC	AGC	TCA	GAG	GCC	AAG	AAC	CAC	ATT	GCC	ACT	GAT	GCT	GTC	AGT	GCT	3110
Thr	Ser	Ser	Glu	Ala	Lys	Asn	His	Ile	Ala	Thr	Asp	Ala	Val	Ser	Ala	
			955			960					965					
GCA	GTG	GGG	AAC	CTG	ACA	AAG	CCA	GCT	CTC	AGT	AGC	CCC	AAG	GAG	AAC	3158
Ala	Val	Gly	Asn	Leu	Thr	Lys	Pro	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Asn	
970					975					980					985	
CAC	GGG	GAC	TTC	ATC	ACT	GAT	CCC	AAC	GTG	TGG	GTC	TCT	GTG	CCC	ATT	3206
His	Gly	Asp	Phe	Ile	Thr	Asp	Pro	Asn	Val	Trp	Val	Ser	Val	Pro	Ile	
				990					995					1000		
GCT	GAG	GGG	GAA	TCT	GAC	CTC	GAC	GAG	CTC	GAG	GAA	GAT	ATG	GAG	CAG	3254
Ala	Glu	Gly	Glu	Ser	Asp	Leu	Asp	Glu	Leu	Glu	Glu	Asp	Met	Glu	Gln	
			1005					1010					1015			

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GCT TCG CAG AGC TCC TGG CAG GAA GAG GAC CCC AAG GGA CAG CAG GAG Ala Ser Gln Ser Ser Trp Gln Glu Glu Asp Pro Lys Gly Gln Gln Glu 1020 1025 1030	3302
CAG TTG CCA CAA GTC CAA AAG TGT GAA AAC CAC CAG GCA GCC AGA AGC Gln Leu Pro Gln Val Gln Lys Cys Glu Asn His Gln Ala Ala Arg Ser 1035 1040 1045	3350
CCA GCC TCC ATG ATG TCC TCT GAG GAC CTG GCT CCA TAC CTG GGT GAG Pro Ala Ser Met Met Ser Ser Glu Asp Leu Ala Pro Tyr Leu Gly Glu 1050 1055 1060 1065	3398
AGC TGG AAG AGG AAG GAT AGC CCT CAG GTC CCT GCC GAG GGA GTG GAT Ser Trp Lys Arg Lys Asp Ser Pro Gln Val Pro Ala Glu Gly Val Asp 1070 1075 1080	3446
GAC ACG AGC TCC TCT GAG GGC AGC ACG GTG GAC TGC CCG GAC CCA GAG Asp Thr Ser Ser Ser Glu Gly Ser Thr Val Asp Cys Pro Asp Pro Glu 1085 1090 1095	3494
GAA ATC CTG AGG AAG ATC CCC GAG CTG GCA CAT GAC CTG GAC GAG CCC Glu Ile Leu Arg Lys Ile Pro Glu Leu Ala His Asp Leu Asp Glu Pro 1100 1105 1110	3542
GAT GAC TGT TTC AGA GAA GGC TGC ACT CGC CGC TGT CCC TGC TGC AAC Asp Asp Cys Phe Arg Glu Gly Cys Thr Arg Arg Cys Pro Cys Cys Asn 1115 1120 1125	3590
GTG AAT ACT AGC AAG TCT CCT TGG GCC ACA GGC TGG CAG GTG CGC AAG Val Asn Thr Ser Lys Ser Pro Trp Ala Thr Gly Trp Gln Val Arg Lys 1130 1135 1140 1145	3638
ACC TGC TAC CGC ATC GTG GAG CAC AGC TGG TTT GAG AGT TTC ATC ATC Thr Cys Tyr Arg Ile Val Glu His Ser Trp Phe Glu Ser Phe Ile Ile 1150 1155 1160	3686
TTC ATG ATC CTG CTC AGC AGT GGA GCG CTG GCC TTT GAG GAT AAC TAC Phe Met Ile Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Asn Tyr 1165 1170 1175	3734
CTG GAA GAG AAA CCC CGA GTG AAG TCC GTG CTG GAG TAC ACT GAC CGA Leu Glu Glu Lys Pro Arg Val Lys Ser Val Leu Glu Tyr Thr Asp Arg 1180 1185 1190	3782
GTG TTC ACC TTC ATC TTC GTC TTT GAG ATG CTG CTC AAG TGG GTA GCC Val Phe Thr Phe Ile Phe Val Phe Glu Met Leu Leu Lys Trp Val Ala 1195 1200 1205	3830
TAT GGC TTC AAA AAG TAT TTC ACC AAT GCC TGG TGC TGG CTG GAC TTC Tyr Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe 1210 1215 1220 1225	3878
CTC ATT GTG AAC ATC TCC CTG ACA AGC CTC ATA GCG AAG ATC CTT GAG Leu Ile Val Asn Ile Ser Leu Thr Ser Leu Ile Ala Lys Ile Leu Glu 1230 1235 1240	3926
TAT TCC GAC GTG GCG TCC ATC AAA GCC CTT CGG ACT CTC CGT GCC CTC Tyr Ser Asp Val Ala Ser Ile Lys Ala Leu Arg Thr Leu Arg Ala Leu 1245 1250 1255	3974
CGA CCG CTG CGG GCT CTG TCT CGA TTC GAA GGC ATG AGG GTA GTG GTG Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val 1260 1265 1270	4022

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GAT Asp	GCC Ala	CTC Leu	GTG Val	GGC Gly	GCC Ala	ATC Ile	CCC Pro	TCC Ser	ATC Ile	ATG Met	AAC Asn	GTC Val	CTC Leu	CTC Leu	GTC Val	4070
1275						1280					1285					
TGC Cys	CTC Leu	ATC Ile	TTC Phe	TGG Trp	CTC Leu	ATC Ile	TTC Phe	AGC Ser	ATC Ile	ATG Met	GGC Gly	GTG Val	AAC Asn	CTC Leu	TTC Phe	4118
1290					1295					1300					1305	
GCC Ala	GGG Gly	AAA Lys	TTT Phe	TCG Ser	AAG Lys	TGC Cys	GTC Val	GAC Asp	ACC Thr	AGA Arg	AAT Asn	AAC Asn	CCA Pro	TTT Phe	TCC Ser	4166
				1310					1315					1320		
AAC Asn	GTG Val	AAT Asn	TCG Ser	ACG Thr	ATG Met	GTG Val	AAT Asn	AAC Asn	AAG Lys	TCC Ser	GAG Glu	TGT Cys	CAC His	AAT Asn	CAA Gln	4214
			1325					1330					1335			
AAC Asn	AGC Ser	ACC Thr	GGC Gly	CAC His	TTC Phe	TTC Phe	TGG Trp	GTC Val	AAC Asn	GTC Val	AAA Lys	GTC Val	AAC Asn	TTC Phe	GAC Asp	4262
			1340				1345					1350				
AAC Asn	GTC Val	GCT Ala	ATG Met	GGC Gly	TAC Tyr	CTC Leu	GCA Ala	CTT Leu	CTT Leu	CAG Gln	GTG Val	GCA Ala	ACC Thr	TTC Phe	AAA Lys	4310
						1360					1365					
GGC Gly	TGG Trp	ATG Met	GAC Asp	ATA Ile	ATG Met	TAT Tyr	GCA Ala	GCT Ala	GTT Val	GAT Asp	TCC Ser	GGA Gly	GAG Glu	ATC Ile	AAC Asn	4358
1370					1375					1380					1385	
AGT Ser	CAG Gln	CCT Pro	AAC Asn	TGG Trp	GAG Glu	AAC Asn	AAC Asn	TTG Leu	TAC Tyr	ATG Met	TAC Tyr	CTG Leu	TAC Tyr	TTC Phe	GTC Val	4406
				1390					1395					1400		
GTT Val	TTC Phe	ATC Ile	ATT Ile	TTC Phe	GGT Gly	GGC Gly	TTC Phe	TTC Phe	ACG Thr	CTG Leu	AAT Asn	CTC Leu	TTT Phe	GTT Val	GGG Gly	4454
				1405				1410					1415			
GTC Val	ATA Ile	ATC Ile	GAC Asp	AAC Asn	TTC Phe	AAC Asn	CAA Gln	CAG Gln	AAA Lys	AAA Lys	AAG Lys	CTA Leu	GGA Gly	GGC Gly	CAG Gln	4502
			1420				1425					1430				
GAC Asp	ATC Ile	TTC Phe	ATG Met	ACA Thr	GAA Glu	GAG Glu	CAG Gln	AAG Lys	AAG Lys	TAC Tyr	TAC Tyr	AAT Asn	GCC Ala	ATG Met	AAG Lys	4550
	1435					1440				1445						
AAG Lys	CTG Leu	GGC Gly	TCC Ser	AAG Lys	AAA Lys	CCC Pro	CAG Gln	AAG Lys	CCC Pro	ATC Ile	CCA Pro	CGG Arg	CCC Pro	CTG Leu	AAT Asn	4598
1450				1455						1460					1465	
AAG Lys	TAC Tyr	CAA Gln	GGC Gly	TTC Phe	GTG Val	TTT Phe	GAC Asp	ATC Ile	GTG Val	ACC Thr	AGG Arg	CAA Gln	GCC Ala	TTT Phe	GAC Asp	4646
				1470					1475					1480		
ATC Ile	ATC Ile	ATC Ile	ATG Met	GTT Val	CTC Leu	ATC Ile	TGC Cys	CTC Leu	AAC Asn	ATG Met	ATC Ile	ACC Thr	ATG Met	ATG Met	GTG Val	4694
			1485					1490					1495			
GAG Glu	ACC Thr	GAC Asp	GAG Glu	CAG Gln	GGC Gly	GAG Glu	GAG Glu	AAG Lys	ACG Thr	AAG Lys	GTT Val	CTG Leu	GGC Gly	AGA Arg	ATC Ile	4742
		1500				1505						1510				
AAC Asn	CAG Gln	TTC Phe	TTT Phe	GTG Val	GCC Ala	GTC Val	TTC Phe	ACG Thr	GGC Gly	GAG Glu	TGT Cys	GTG Val	ATG Met	AAG Lys	ATG Met	4790
		1515				1520					1525					

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TTC	GCC	CTG	CGA	CAG	TAC	TAC	TTC	ACC	AAC	GGC	TGG	AAC	GTG	TTC	GAC	4838
Phe	Ala	Leu	Arg	Gln	Tyr	Tyr	Phe	Thr	Asn	Gly	Trp	Asn	Val	Phe	Asp	
1530					1535					1540					1545	
TTC	ATA	GTG	GTG	ATC	CTG	TCC	ATT	GGG	AGT	CTG	CTG	TTT	TCT	GCA	ATC	4886
Phe	Ile	Val	Val	Ile	Leu	Ser	Ile	Gly	Ser	Leu	Leu	Phe	Ser	Ala	Ile	
				1550					1555					1560		
CTT	AAG	TCA	CTG	GAA	AAC	TAC	TTC	TCC	CCG	ACG	CTC	TTC	CGG	GTC	ATC	4934
Leu	Lys	Ser	Leu	Glu	Asn	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	Arg	Val	Ile	
			1565					1570					1575			
CGT	CTG	GCC	AGG	ATC	GGC	CGC	ATC	CTC	AGG	CTG	ATC	CGA	GCA	GCC	AAG	4982
Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	Leu	Ile	Arg	Ala	Ala	Lys	
		1580					1585					1590				
GGG	ATT	CGC	ACG	CTG	CTC	TTC	GCC	CTC	ATG	ATG	TCC	CTG	CCC	GCC	CTC	5030
Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	Met	Met	Ser	Leu	Pro	Ala	Leu	
	1595					1600					1605					
TTC	AAC	ATC	GGC	CTC	CTC	CTC	TTC	CTC	GTC	ATG	TTC	ATC	TAC	TCC	ATC	5078
Phe	Asn	Ile	Gly	Leu	Leu	Leu	Phe	Leu	Val	Met	Phe	Ile	Tyr	Ser	Ile	
1610				1615					1620						1625	
TTC	GGC	ATG	GCC	AGC	TTC	GCT	AAC	GTC	GTG	GAC	GAG	GCC	GGC	ATC	GAC	5126
Phe	Gly	Met	Ala	Ser	Phe	Ala	Asn	Val	Val	Asp	Glu	Ala	Gly	Ile	Asp	
			1630					1635					1640			
GAC	ATG	TTC	AAC	TTC	AAG	ACC	TTT	GGC	AAC	AGC	ATG	CTG	TGC	CTG	TTC	5174
Asp	Met	Phe	Asn	Phe	Lys	Thr	Phe	Gly	Asn	Ser	Met	Leu	Cys	Leu	Phe	
			1645					1650					1655			
CAG	ATC	ACC	ACC	TCG	GCC	GGC	TGG	GAC	GGC	CTC	CTC	AGC	CCC	ATC	CTC	5222
Gln	Ile	Thr	Thr	Ser	Ala	Gly	Trp	Asp	Gly	Leu	Leu	Ser	Pro	Ile	Leu	
		1660					1665					1670				
AAC	ACG	GGG	CCT	CCC	TAC	TGC	GAC	CCC	AAC	CTG	CCC	AAC	AGC	AAC	GGC	5270
Asn	Thr	Gly	Pro	Pro	Tyr	Cys	Asp	Pro	Asn	Leu	Pro	Asn	Ser	Asn	Gly	
	1675					1680				1685						
TCC	CGG	GGG	AAC	TGC	GGG	AGC	CCG	GCG	GTG	GGC	ATC	ATC	TTC	TTC	ACC	5318
Ser	Arg	Gly	Asn	Cys	Gly	Ser	Pro	Ala	Val	Gly	Ile	Ile	Phe	Phe	Thr	
1690				1695					1700						1705	
ACC	TAC	ATC	ATC	ATC	TCC	TTC	CTC	ATC	GTG	GTC	AAC	ATG	TAC	ATC	GCA	5366
Thr	Tyr	Ile	Ile	Ile	Ser	Phe	Leu	Ile	Val	Val	Asn	Met	Tyr	Ile	Ala	
				1710					1715					1720		
GTG	ATT	CTG	GAG	AAC	TTC	AAC	GTA	GCC	ACC	GAG	GAG	AGC	ACG	GAG	CCC	5414
Val	Ile	Leu	Glu	Asn	Phe	Asn	Val	Ala	Thr	Glu	Glu	Ser	Thr	Glu	Pro	
			1725				1730						1735			
CTG	AGC	GAG	GAC	GAC	TTC	GAC	ATG	TTC	TAT	GAG	ACC	TGG	GAG	AAG	TTC	5462
Leu	Ser	Glu	Asp	Asp	Phe	Asp	Met	Phe	Tyr	Glu	Thr	Trp	Glu	Lys	Phe	
		1740					1745					1750				
GAC	CCG	GAG	GCC	ACC	CAG	TTC	ATT	GCC	TTT	TCT	GCC	CTC	TCA	GAC	TTC	5510
Asp	Pro	Glu	Ala	Thr	Gln	Phe	Ile	Ala	Phe	Ser	Ala	Leu	Ser	Asp	Phe	
	1755					1760					1765					
GCG	GAC	ACG	CTC	TCC	GGC	CCT	CTT	AGA	ATC	CCC	AAA	CCC	AAC	CAG	AAT	5558
Ala	Asp	Thr	Leu	Ser	Gly	Pro	Leu	Arg	Ile	Pro	Lys	Pro	Asn	Gln	Asn	
1770					1775					1780					1785	

ATA TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT AAG ATC CAC Ile Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His 1790 1795 1800	5606
TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG GGA GAA TCC Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser 1805 1810 1815	5654
GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG TTT ATG GCG Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala 1820 1825 1830	5702
ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg 1835 1840 1845	5750
TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg 1850 1855 1860 1865	5798
AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val 1870 1875 1880	5846
CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC ATT Pro Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ile 1885 1890 1895	5894
ACA TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser 1900 1905 1910	5942
GCT ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser 1915 1920 1925	5990
GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG Asp Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu 1930 1935 1940 1945	6038
GTC GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln 1950 1955	6084
CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG	6144
AGGTGGCACC AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA	6204
ATGGGGACAT CCTTGAGAAA GCCCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT	6264
CCATTCTGAC GTCCCTTCCG AGTTCCCAGA AGATGTCATT GCTCCCTTCT GTTTGTGACC	6324
AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG	6384
TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTTGGTACT GAGAATTAGG GTTTGCATGA	6444
CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTAA	6504
AAGTTAAAAA AAAAAAAAAA	6524

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1957 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu Leu Pro Phe Ala Ser Val Gly Thr Thr Asn Phe Arg Arg Phe
 1           5           10
Thr Pro Glu Ser Leu Ala Glu Ile Glu Lys Gln Ile Ala Ala His Arg
          20           25           30
Ala Ala Lys Lys Ala Arg Thr Lys His Arg Gly Gln Glu Asp Lys Gly
          35           40           45
Glu Lys Pro Arg Pro Gln Leu Asp Leu Lys Asp Cys Asn Gln Leu Pro
          50           55           60
Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
65           70           75           80
Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
          85           90           95
Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
          100          105          110
Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
          115          120          125
His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
          130          135          140
Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
145          150          155          160
Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
          165          170          175
Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
          180          185          190
Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
          195          200          205
Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
210          215          220
Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
225          230          235          240
His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
          245          250          255
Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
          260          265          270
Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
          275          280          285

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Leu Ser Ser Glu Met Ala Glu Tyr Val Ser Ile Lys Pro Gly Thr Thr
 290 295 300
 Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320
 Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 325 330 335
 Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350
 Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
 355 360 365
 Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
 370 375 380
 Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
 385 390 395 400
 Glu Gln Ser Gln Ala Thr Ile Ala Glu Ile Glu Ala Lys Glu Lys Lys
 405 410 415
 Phe Gln Glu Ala Leu Glu Val Leu Gln Lys Glu Gln Glu Val Leu Ala
 420 425 430
 Ala Leu Gly Ile Asp Thr Thr Ser Leu Gln Ser His Ser Gly Ser Pro
 435 440 445
 Leu Ala Ser Lys Asn Ala Asn Glu Arg Arg Pro Arg Val Lys Ser Arg
 450 455 460
 Val Ser Glu Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro
 465 470 475 480
 Tyr Asn Gln Arg Arg Met Ser Phe Leu Gly Leu Ser Ser Gly Arg Arg
 485 490 495
 Arg Ala Ser His Gly Ser Val Phe His Phe Arg Ala Pro Ser Gln Asp
 500 505 510
 Ile Ser Phe Pro Asp Gly Ile Thr Pro Asp Asp Gly Val Phe His Gly
 515 520 525
 Asp Gln Glu Ser Arg Arg Gly Ser Ile Leu Leu Gly Arg Gly Ala Gly
 530 535 540
 Gln Thr Gly Pro Leu Pro Arg Ser Pro Leu Pro Gln Ser Pro Asn Pro
 545 550 555 560
 Gly Arg Arg His Gly Glu Glu Gly Gln Leu Gly Val Pro Thr Gly Glu
 565 570 575
 Leu Thr Ala Gly Ala Pro Glu Gly Pro Ala Leu His Thr Thr Gly Gln
 580 585 590
 Lys Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln
 595 600 605
 Arg Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu
 610 615 620

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Glu 625	Glu	Ser	Lys	Leu	Lys 630	Cys	Pro	Pro	Cys	Leu 635	Ile	Ser	Phe	Ala	Gln 640
Lys	Tyr	Leu	Ile	Trp 645	Glu	Cys	Cys	Pro	Lys 650	Trp	Arg	Lys	Phe	Lys	Met 655
Ala	Leu	Phe	Glu 660	Leu	Val	Thr	Asp	Pro 665	Phe	Ala	Glu	Leu	Thr 670	Ile	Thr
Leu	Cys	Ile 675	Val	Val	Asn	Thr	Val 680	Phe	Met	Ala	Met	Glu 685	His	Tyr	Pro
Met	Thr 690	Asp	Ala	Phe	Asp	Ala 695	Met	Leu	Gln	Ala	Gly 700	Asn	Ile	Val	Phe
Thr 705	Val	Phe	Phe	Thr	Met 710	Glu	Met	Ala	Phe	Lys 715	Ile	Ile	Ala	Phe	Asp 720
Pro	Tyr	Tyr	Tyr	Phe 725	Gln	Lys	Lys	Trp	Asn 730	Ile	Phe	Asp	Cys	Val 735	Ile
Val	Thr	Val	Ser 740	Leu	Leu	Glu	Leu	Ser 745	Ala	Ser	Lys	Lys	Gly 750	Ser	Leu
Ser	Val	Leu 755	Arg	Thr	Leu	Arg	Leu 760	Leu	Arg	Val	Phe	Lys 765	Leu	Ala	Lys
Ser	Trp 770	Pro	Thr	Leu	Asn	Thr 775	Leu	Ile	Lys	Ile	Ile 780	Gly	Asn	Ser	Val
Gly 785	Ala	Leu	Gly	Asn	Leu 790	Thr	Phe	Ile	Leu	Ala 795	Ile	Ile	Val	Phe	Ile 800
Phe	Ala	Leu	Val	Gly 805	Lys	Gln	Leu	Leu	Ser 810	Glu	Asp	Tyr	Gly	Cys	Arg 815
Lys	Asp	Gly	Val 820	Ser	Val	Trp	Asn	Gly 825	Glu	Lys	Leu	Arg	Trp 830	His	Met
Cys	Asp	Phe 835	Phe	His	Ser	Phe	Leu 840	Val	Val	Phe	Arg	Ile 845	Leu	Cys	Gly
Glu	Trp 850	Ile	Glu	Asn	Met	Trp 855	Val	Cys	Met	Glu	Val 860	Ser	Gln	Lys	Ser
Ile 865	Cys	Leu	Ile	Leu	Phe 870	Leu	Thr	Val	Met	Val 875	Leu	Gly	Asn	Leu	Val 880
Val	Leu	Asn	Leu	Phe 885	Ile	Ala	Leu	Leu	Leu 890	Asn	Ser	Phe	Ser	Ala 895	Asp
Asn	Leu	Thr	Ala 900	Pro	Glu	Asp	Asp	Gly 905	Glu	Val	Asn	Asn	Leu 910	Gln	Leu
Ala	Leu	Ala	Arg	Ile	Gln	Val	Leu	Gly	His	Arg	Ala	Ser 925	Arg	Ala	Ser
Ala	Ser 930	Tyr	Ile	Ser	Ser	His 935	Cys	Arg	Phe	His	Trp 940	Pro	Lys	Val	Glu
Thr 945	Gln	Leu	Gly	Met	Lys 950	Pro	Pro	Leu	Thr	Ser 955	Ser	Glu	Ala	Lys	Asn 960

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His Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys
 965 970 975
 Pro Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp
 980 985 990
 Pro Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu
 995 1000 1005
 Asp Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln
 1010 1015 1020
 Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys
 1025 1030 1035 1040
 Cys Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser
 1045 1050 1055
 Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser
 1060 1065 1070
 Pro Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly
 1075 1080 1085
 Ser Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro
 1090 1095 1100
 Glu Leu Ala His Asp Leu Asp Glu Pro Asp Asp Cys Phe Arg Glu Gly
 1105 1110 1115 1120
 Cys Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro
 1125 1130 1135
 Trp Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu
 1140 1145 1150
 His Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser
 1155 1160 1165
 Gly Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val
 1170 1175 1180
 Lys Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val
 1185 1190 1195 1200
 Phe Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe
 1205 1210 1215
 Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu
 1220 1225 1230
 Thr Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile
 1235 1240 1245
 Lys Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser
 1250 1255 1260
 Arg Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile
 1265 1270 1275 1280
 Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile
 1285 1290 1295
 Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys
 1300 1305 1310

Val Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val
 1315 1320 1325
 Asn Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe
 1330 1335 1340
 Trp Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu
 1345 1350 1355 1360
 Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr
 1365 1370 1375
 Ala Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn
 1380 1385 1390
 Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly
 1395 1400 1405
 Phe Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn
 1410 1415 1420
 Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu
 1425 1430 1435 1440
 Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro
 1445 1450 1455
 Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe
 1460 1465 1470
 Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile
 1475 1480 1485
 Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu
 1490 1495 1500
 Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val
 1505 1510 1515 1520
 Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr
 1525 1530 1535
 Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser
 1540 1545 1550
 Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr
 1555 1560 1565
 Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg
 1570 1575 1580
 Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe
 1585 1590 1595 1600
 Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu
 1605 1610 1615
 Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala
 1620 1625 1630
 Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr
 1635 1640 1645

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Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly
 1650 1655 1660
 Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys
 1665 1670 1675 1680
 Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser
 1685 1690 1695
 Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe
 1700 1705 1710
 Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn
 1715 1720 1725
 Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp
 1730 1735 1740
 Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe
 1745 1750 1755 1760
 Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro
 1765 1770 1775
 Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu
 1780 1785 1790
 Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala
 1795 1800 1805
 Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys
 1810 1815 1820
 Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser
 1825 1830 1835 1840
 Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser
 1845 1850 1855
 Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser
 1860 1865 1870
 Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly
 1875 1880 1885
 Val Ser Leu Pro Gly Glu Gly Tyr Ile Thr Phe Met Ala Asn Ser Gly
 1890 1895 1900
 Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser
 1905 1910 1915 1920
 Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro
 1925 1930 1935
 Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn
 1940 1945 1950
 Ser Pro Gly Pro Gln
 1955

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 561..2126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CTGGGAGAGA AAGCGTCTCG CCTAGCGACT CCCAGAGCTT TAAGCCGGGA AGGGACAAGC      60
GTCAGGACAT CTCAGAATCC CGAACCTTCT AGGGAGGGAG GTTCTTACCT CCATGCTTCC      120
CGTAGGAACC TAATCCCAAT TATTTAGCTG TATTTATAAT ACAAATATG AATGTTAAAT      180
GTACAAAATG CTTTCCAGC ATGCCTGCAT CTCCTCCTAG AGTCCTGTTC CCAAGCCCTC      240
TCTACTCTCA GTACTGTAGA AAAGAAATAA GCTTTACGTG AGAAACCCAG GCACTGGATC      300
TTATCCAGGT GCTCACCTCA GAGTCTTTAG TGGGTGTAGC GCTGTGGTAG AGCATTTGGT      360
TATAGATACA AACCCAGGGC AGGGAGACTG CAGTGGCCAT TCTCTCCCAG GCCAGACGTG      420
CCCTGATCCT TCCCACAGAG ATGAGAAGGC TGGAACCAGA AACTCAGGT TTTGGCTTCT      480
CTTGGGGGAG GAGAGGTAAT CTTGTTACTT TAATAACATC AGTGTGTCCC TCTCCTCTAC      540
TAGGAGGCCA GGACATCTTC ATG ACA GAA GAG CAG AAG AAG TAC TAC AAT      590
                Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn
                  1             5             10

GCC ATG AAG AAG CTG GGC TCC AAG AAA CCC CAG AAG CCC ATC CCA CGG      638
Ala Met Lys Lys Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg
                  15             20             25

CCC CTG AAT AAG TAC CAA GGC TTC GTG TTT GAC ATC GTG ACC AGG CAA      686
Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe Asp Ile Val Thr Arg Gln
                  30             35             40

GCC TTT GAC ATC ATC ATC ATG GTT CTC ATC TGC CTC AAC ATG ATC ACC      734
Ala Phe Asp Ile Ile Ile Met Val Leu Ile Cys Leu Asn Met Ile Thr
                  45             50             55

ATG ATG GTG GAG ACC GAC GAG CAG GGC GAG GAG AAG ACG AAG GTT CTG      782
Met Met Val Glu Thr Asp Glu Gln Gly Glu Glu Lys Thr Lys Val Leu
                  60             65             70

GGC AGA ATC AAC CAG TTC TTT GTG GCC GTC TTC ACG GGC GAG TGT GTG      830
Gly Arg Ile Asn Gln Phe Phe Val Ala Val Phe Thr Gly Glu Cys Val
                  75             80             85

ATG AAG ATG TTC GCC CTG CGA CAG TAC TAC TTC ACC AAC GGC TGG AAC      878
Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn
                  95             100             105

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GTG	TTC	GAC	TTC	ATA	GTG	GTG	ATC	CTG	TCC	ATT	GGG	AGT	CTG	CTG	TTT	926
Val	Phe	Asp	Phe	Ile	Val	Val	Ile	Leu	Ser	Ile	Gly	Ser	Leu	Leu	Phe	
			110					115					120			
TCT	GCA	ATC	CTT	AAG	TCA	CTG	GAA	AAC	TAC	TTC	TCC	CCG	ACG	CTC	TTC	974
Ser	Ala	Ile	Leu	Lys	Ser	Leu	Glu	Asn	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	
		125					130					135				
CGG	GTC	ATC	CGT	CTG	GCC	AGG	ATC	GGC	CGC	ATC	CTC	AGG	CTG	ATC	CGA	1022
Arg	Val	Ile	Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	Leu	Ile	Arg	
	140					145					150					
GCA	GCC	AAG	GGG	ATT	CGC	ACG	CTG	CTC	TTC	GCC	CTC	ATG	ATG	TCC	CTG	1070
Ala	Ala	Lys	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	Met	Met	Ser	Leu	
155					160				165						170	
CCC	GCC	CTC	TTC	AAC	ATC	GGC	CTC	CTC	CTC	TTC	CTC	GTC	ATG	TTC	ATC	1118
Pro	Ala	Leu	Phe	Asn	Ile	Gly	Leu	Leu	Leu	Phe	Leu	Val	Met	Phe	Ile	
				175					180					185		
TAC	TCC	ATC	TTC	GGC	ATG	GCC	AGC	TTC	GCT	AAC	GTC	GTG	GAC	GAG	GCC	1166
Tyr	Ser	Ile	Phe	Gly	Met	Ala	Ser	Phe	Ala	Asn	Val	Val	Asp	Glu	Ala	
			190					195					200			
GGC	ATC	GAC	GAC	ATG	TTC	AAC	TTC	AAG	ACC	TTT	GGC	AAC	AGC	ATG	CTG	1214
Gly	Ile	Asp	Asp	Met	Phe	Asn	Phe	Lys	Thr	Phe	Gly	Asn	Ser	Met	Leu	
		205					210					215				
TGC	CTG	TTC	CAG	ATC	ACC	ACC	TCG	GCC	GGC	TGG	GAC	GGC	CTC	CTC	AGC	1262
Cys	Leu	Phe	Gln	Ile	Thr	Thr	Ser	Ala	Gly	Trp	Asp	Gly	Leu	Leu	Ser	
	220					225					230					
CCC	ATC	CTC	AAC	ACG	GGG	CCT	CCC	TAC	TGC	GAC	CCC	AAC	CTG	CCC	AAC	1310
Pro	Ile	Leu	Asn	Thr	Gly	Pro	Pro	Tyr	Cys	Asp	Pro	Asn	Leu	Pro	Asn	
235					240				245						250	
AGC	AAC	GGC	TCC	CGG	GGG	AAC	TGC	GGG	AGC	CCG	GCG	GTG	GGC	ATC	ATC	1358
Ser	Asn	Gly	Ser	Arg	Gly	Asn	Cys	Gly	Ser	Pro	Ala	Val	Gly	Ile	Ile	
				255				260						265		
TTC	TTC	ACC	ACC	TAC	ATC	ATC	ATC	TCC	TTC	CTC	ATC	GTG	GTC	AAC	ATG	1406
Phe	Phe	Thr	Thr	Tyr	Ile	Ile	Ile	Ser	Phe	Leu	Ile	Val	Val	Asn	Met	
			270					275					280			
TAC	ATC	GCA	GTG	ATT	CTG	GAG	AAC	TTC	AAC	GTA	GCC	ACC	GAG	GAG	AGC	1454
Tyr	Ile	Ala	Val	Ile	Leu	Glu	Asn	Phe	Asn	Val	Ala	Thr	Glu	Glu	Ser	
		285					290					295				
ACG	GAG	CCC	CTG	AGC	GAG	GAC	GAC	TTC	GAC	ATG	TTC	TAT	GAG	ACC	TGG	1502
Thr	Glu	Pro	Leu	Ser	Glu	Asp	Asp	Phe	Asp	Met	Phe	Tyr	Glu	Thr	Trp	
	300					305					310					
GAG	AAG	TTC	GAC	CCG	GAG	GCC	ACC	CAG	TTC	ATT	GCC	TTT	TCT	GCC	CTC	1550
Glu	Lys	Phe	Asp	Pro	Glu	Ala	Thr	Gln	Phe	Ile	Ala	Phe	Ser	Ala	Leu	
315					320				325						330	
TCA	GAC	TTC	GCG	GAC	ACG	CTC	TCC	GGC	CCT	CTT	AGA	ATC	CCC	AAA	CCC	1598
Ser	Asp	Phe	Ala	Asp	Thr	Leu	Ser	Gly	Pro	Leu	Arg	Ile	Pro	Lys	Pro	
				335				340						345		
AAC	CAG	AAT	ATA	TTA	ATC	CAG	ATG	GAC	CTG	CCG	TTG	GTC	CCC	GGG	GAT	1646
Asn	Gln	Asn	Ile	Leu	Ile	Gln	Met	Asp	Leu	Pro	Leu	Val	Pro	Gly	Asp	
			350					355					360			

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AAG ATC CAC TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG Lys Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu 365 370 375	1694
GGA GAA TCC GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys 380 385 390	1742
TTT ATG GCG ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC Phe Met Ala Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr 395 400 405 410	1790
ACC CTC CGG TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys 415 420 425	1838
GCC TAC CGG AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC Ala Tyr Arg Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr 430 435 440	1886
CTG CAT GTG CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA Leu His Val Pro Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu 445 450 455	1934
GGC TAC ATT ACA TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA Gly Tyr Ile Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu 460 465 470	1982
ACT GCC TCT GCT ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg 475 480 485 490	2030
GGC CTG AGT GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT Gly Leu Ser Asp Arg Ala Asn Ile Asn Ser Ser Ser Met Gln Asn 495 500 505	2078
GAA GAT GAG GTC GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT Glu Asp Glu Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln 510 515 520	2133
CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG	2193
AGGTGGCACC AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA	2253
ATGGGGACAT CCTTGAGAAA GCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT	2313
CCATTCTGAC GTCCCTTCCG AGTTCCCAGA AGATGTCATT GCTCCCTTCT GTTTGTGACC	2373
AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG	2433
TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTGTTGTTACT GAGAATTAGG GTTTGCATGA	2493
CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTTA	2553
AAGTTAAAAA AAAAAAAAAA	2573

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly
 1           5           10           15
Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln
          20           25           30
Gly Phe Val Phe Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile
          35           40           45
Met Val Leu Ile Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp
          50           55           60
Glu Gln Gly Glu Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe
          65           70           75           80
Phe Val Ala Val Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu
          85           90           95
Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val
          100          105          110
Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser
          115          120          125
Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala
          130          135          140
Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg
          145          150          155          160
Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile
          165          170          175
Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met
          180          185          190
Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe
          195          200          205
Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr
          210          215          220
Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly
          225          230          235          240
Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly
          245          250          255
Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile
          260          265          270
Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu
          275          280          285

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Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu
 290 295 300
 Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu
 305 310 315 320
 Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr
 325 330 335
 Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile
 340 345 350
 Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp
 355 360 365
 Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu
 370 375 380
 Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu
 385 390 395 400
 Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln
 405 410 415
 Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met
 420 425 430
 Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala
 435 440 445
 Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ile Thr Phe Met
 450 455 460
 Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser
 465 470 475 480
 Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala
 485 490 495
 Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala
 500 505 510
 Lys Glu Gly Asn Ser Pro Gly Pro Gln
 515 520

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 204..6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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TAGCTTGCTT	CTGCTAATGC	TACCCCAGGC	CTTTAGACAG	AGAACAGATG	GCAGATGGAG	60
TTTCTTATTG	CCATGCGCAA	ACGCTGAGCC	CACCTCATGA	TCCCGGACCC	CATGGTTTTTC	120
AGTAGACAAC	CTGGGCTAAG	AAGAGATCTC	CGACCTTATA	GAGCAGCAAA	GAGTGTAAT	180
TCTTCCCCAA	GAAGAATGAG	AAG	ATG	GAG	CTC	230
		Met	Glu	Leu	Pro	
		1			5	
ACT ACC AAT TTC AGA CGG TTC ACT CCA GAG TCA CTG GCA GAG ATC GAG	278					
Thr Thr Asn Phe Arg Arg Phe Thr Pro Glu Ser Leu Ala Glu Ile Glu						
10 15 20 25						
AAG CAG ATT GCT GCT CAC CGG GCA GCC AAG AAG GCC AGA ACC AAG CAC	326					
Lys Gln Ile Ala Ala His Arg Ala Ala Lys Lys Ala Arg Thr Lys His						
30 35 40						
AGA GGA CAG GAG GAC AAG GGC GAG AAG CCC AGG CCT CAG CTG GAC TTG	374					
Arg Gly Gln Glu Asp Lys Gly Glu Lys Pro Arg Pro Gln Leu Asp Leu						
45 50 55						
AAA GAC TGT AAC CAG CTG CCC AAG TTC TAT GGT GAG CTC CCA GCA GAA	422					
Lys Asp Cys Asn Gln Leu Pro Lys Phe Tyr Gly Glu Leu Pro Ala Glu						
60 65 70						
CTG GTC GGG GAG CCC CTG GAG GAC CTA GAC CCT TTC TAC AGC ACA CAC	470					
Leu Val Gly Glu Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr His						
75 80 85						
CGG ACA TTC ATG GTG TTG AAT AAA AGC AGG ACC ATT TCC AGA TTC AGT	518					
Arg Thr Phe Met Val Leu Asn Lys Ser Arg Thr Ile Ser Arg Phe Ser						
90 95 100 105						
GCC ACT TGG GCC CTG TGG CTC TTC AGT CCC TTC AAC CTG ATC AGA AGA	566					
Ala Thr Trp Ala Leu Trp Leu Phe Ser Pro Phe Asn Leu Ile Arg Arg						
110 115 120						
ACA GCC ATC AAA GTG TCT GTC CAT TCC TGG TTC TCC ATA TTC ATC ACC	614					
Thr Ala Ile Lys Val Ser Val His Ser Trp Phe Ser Ile Phe Ile Thr						
125 130 135						
ATC ACT ATT TTG GTC AAC TGC GTG TGC ATG ACC CGA ACT GAT CTT CCA	662					
Ile Thr Ile Leu Val Asn Cys Val Cys Met Thr Arg Thr Asp Leu Pro						
140 145 150						
GAG AAA GTC GAG TAC GTC TTC ACT GTC ATT TAC ACC TTC GAG GCT CTG	710					
Glu Lys Val Glu Tyr Val Phe Thr Val Ile Tyr Thr Phe Glu Ala Leu						
155 160 165						
ATT AAG ATA CTG GCA AGA GGG TTT TGT CTA AAT GAG TTC ACT TAT CTT	758					
Ile Lys Ile Leu Ala Arg Gly Phe Cys Leu Asn Glu Phe Thr Tyr Leu						
170 175 180 185						
CGA GAT CCG TGG AAC TGG CTG GAC TTC AGT GTC ATT ACC TTG GCG TAT	806					
Arg Asp Pro Trp Asn Trp Leu Asp Phe Ser Val Ile Thr Leu Ala Tyr						
190 195 200						
GTG GGT GCA GCG ATA GAC CTC CGA GGA ATC TCA GGC CTG CGG ACA TTC	854					
Val Gly Ala Ala Ile Asp Leu Arg Gly Ile Ser Gly Leu Arg Thr Phe						
205 210 215						

71

CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG	902
Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys	
		220					225					230				
GTC	ATC	GTG	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG	950
Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	
	235					240					245					
ACT	ATC	CTC	ACA	GTC	TTC	TGC	CTG	AGC	GTC	TTC	GCC	TTG	GTG	GGC	CTG	998
Thr	Ile	Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	
250					255					260					265	
CAG	CTC	TTT	AAG	GGG	AAC	CTT	AAG	AAC	AAA	TGC	ATC	AGG	AAC	GGA	ACA	1046
Gln	Leu	Phe	Lys	Gly	Asn	Leu	Lys	Asn	Lys	Cys	Ile	Arg	Asn	Gly	Thr	
				270					275					280		
GAT	CCC	CAC	AAG	GCT	GAC	AAC	CTC	TCA	TCT	GAA	ATG	GCA	GAA	TAC	ATC	1094
Asp	Pro	His	Lys	Ala	Asp	Asn	Leu	Ser	Ser	Glu	Met	Ala	Glu	Tyr	Ile	
			285					290					295			
TTC	ATC	AAG	CCT	GGT	ACT	ACG	GAT	CCC	TTA	CTG	TGC	GGC	AAT	GGG	TCT	1142
Phe	Ile	Lys	Pro	Gly	Thr	Thr	Asp	Pro	Leu	Leu	Cys	Gly	Asn	Gly	Ser	
		300					305					310				
GAT	GCT	GGT	CAC	TGC	CCT	GGA	GGC	TAT	GTC	TGC	CTG	AAA	ACT	CCT	GAC	1190
Asp	Ala	Gly	His	Cys	Pro	Gly	Gly	Tyr	Val	Cys	Leu	Lys	Thr	Pro	Asp	
	315					320					325					
AAC	CCG	GAT	TTT	AAC	TAC	ACC	AGC	TTT	GAT	TCC	TTT	GCG	TGG	GCA	TTC	1238
Asn	Pro	Asp	Phe	Asn	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	Ala	Phe	
330					335					340					345	
CTC	TCA	CTG	TTC	CGC	CTC	ATG	ACG	CAG	GAC	TCC	TGG	GAG	CGC	CTG	TAC	1286
Leu	Ser	Leu	Phe	Arg	Leu	Met	Thr	Gln	Asp	Ser	Trp	Glu	Arg	Leu	Tyr	
				350					355					360		
CAG	CAG	ACA	CTC	CGG	GCT	TCT	GGG	AAA	ATG	TAC	ATG	GTC	TTT	TTC	GTG	1334
Gln	Gln	Thr	Leu	Arg	Ala	Ser	Gly	Lys	Met	Tyr	Met	Val	Phe	Phe	Val	
			365					370					375			
CTG	GTT	ATT	TTC	CTT	GGA	TCG	TTC	TAC	CTG	GTC	AAT	TTG	ATC	TTG	GCC	1382
Leu	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	
		380					385					390				
GTG	GTC	ACC	ATG	GCG	TAT	GAA	GAG	CAG	AGC	CAG	GCA	ACA	ATT	GCA	GAA	1430
Val	Val	Thr	Met	Ala	Tyr	Glu	Glu	Gln	Ser	Gln	Ala	Thr	Ile	Ala	Glu	
	395					400					405					
ATC	GAA	GCC	AAG	GAA	AAA	AAG	TTC	CAG	GAA	GCC	CTT	GAG	GTG	CTG	CAG	1478
Ile	Glu	Ala	Lys	Glu	Lys	Lys	Phe	Gln	Glu	Ala	Leu	Glu	Val	Leu	Gln	
410					415					420					425	
AAG	GAA	CAG	GAG	GTG	CTG	GCA	GCC	CTG	GGG	ATT	GAC	ACG	ACC	TCG	CTC	1526
Lys	Glu	Gln	Glu	Val	Leu	Ala	Ala	Leu	Gly	Ile	Asp	Thr	Thr	Ser	Leu	
				430					435					440		
CAG	TCC	CAC	AGT	GGA	TCA	CCC	TTA	GCC	TCC	AAA	AAC	GCC	AAT	GAG	AGA	1574
Gln	Ser	His	Ser	Gly	Ser	Pro	Leu	Ala	Ser	Lys	Asn	Ala	Asn	Glu	Arg	
			445					450					455			
AGA	CCC	AGG	GTG	AAA	TCA	AGG	GTG	TCA	GAG	GGC	TCC	ACG	GAT	GAC	AAC	1622
Arg	Pro	Arg	Val	Lys	Ser	Arg	Val	Ser	Glu	Gly	Ser	Thr	Asp	Asp	Asn	
		460					465					470				

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AGG Arg	TCA Ser	CCC Pro	CAA Gln	TCT Ser	GAC Asp	CCT Pro	TAC Tyr	AAC Asn	CAG Gln	CGC Arg	AGG Arg	ATG Met	TCT Ser	TTC Phe	CTA Leu	1670
475						480					485					
GGC Gly	CTG Leu	TCT Ser	TCA Ser	GGA Gly	AGA Arg	CGC Arg	AGG Arg	GCT Ala	AGC Ser	CAC His	GGC Gly	AGT Ser	GTG Val	TTC Phe	CAC His	1718
490					495					500					505	
TTC Phe	CGA Arg	GCG Ala	CCC Pro	AGC Ser	CAA Gln	GAC Asp	ATC Ile	TCA Ser	TTT Phe	CCT Pro	GAC Asp	GGG Gly	ATC Ile	ACC Thr	CCT Pro	1766
				510					515					520		
GAT Asp	GAT Asp	GGG Gly	GTC Val	TTT Phe	CAC His	GGA Gly	GAC Asp	CAG Gln	GAA Glu	AGC Ser	CGT Arg	CGA Arg	GGT Gly	TCC Ser	ATA Ile	1814
			525					530					535			
TTG Leu	CTG Leu	GGC Gly	AGG Arg	GGT Gly	GCT Ala	GGG Gly	CAG Gln	ACA Thr	GGT Gly	CCA Pro	CTC Leu	CCC Pro	AGG Arg	AGC Ser	CCA Pro	1862
		540					545					550				
CTG Leu	CCT Pro	CAG Gln	TCC Ser	CCC Pro	AAC Asn	CCT Pro	GGC Gly	CGT Arg	AGA Arg	CAT His	GGA Gly	GAA Glu	GAG Glu	GGA Gly	CAG Gln	1910
	555					560					565					
CTC Leu	GGA Gly	GTG Val	CCC Pro	ACT Thr	GGT Gly	GAG Glu	CTT Leu	ACC Thr	GCT Ala	GGA Gly	GCG Ala	CCT Pro	GAA Glu	GGC Gly	CCG Pro	1958
570					575					580					585	
GCA Ala	CTC Leu	GAC Asp	ACT Thr	ACA Thr	GGG Gly	CAG Gln	AAG Lys	AGC Ser	TTC Phe	CTG Leu	TCT Ser	GCG Ala	GGC Gly	TAC Tyr	TTG Leu	2006
				590					595					600		
AAC Asn	GAA Glu	CCT Pro	TTC Phe	CGA Arg	GCA Ala	CAG Gln	AGG Arg	GCC Ala	ATG Met	AGC Ser	GTT Val	GTC Val	AGT Ser	ATC Ile	ATG Met	2054
			605					610					615			
ACT Thr	TCT Ser	GTC Val	ATT Ile	GAG Glu	GAG Glu	CTT Leu	GAA Glu	GAG Glu	TCT Ser	AAG Lys	CTG Leu	AAG Lys	TGC Cys	CCA Pro	CCC Pro	2102
		620					625					630				
TGC Cys	TTG Leu	ATC Ile	AGC Ser	TTC Phe	GCT Ala	CAG Gln	AAG Lys	TAT Tyr	CTG Leu	ATC Ile	TGG Trp	GAG Glu	TGC Cys	TGC Cys	CCC Pro	2150
	635					640					645					
AAG Lys	TGG Trp	AGG Arg	AAG Lys	TTC Phe	AAG Lys	ATG Met	GCG Ala	CTG Leu	TTC Phe	GAG Glu	CTG Leu	GTG Val	ACT Thr	GAC Asp	CCC Pro	2198
650					655					660					665	
TTC Phe	GCA Ala	GAG Glu	CTT Leu	ACC Thr	ATC Ile	ACC Thr	CTC Leu	TGC Cys	ATC Ile	GTG Val	GTG Val	AAC Asn	ACC Thr	GTC Val	TTC Phe	2246
				670					675					680		
ATG Met	GCC Ala	ATG Met	GAG Glu	CAC His	TAC Tyr	CCC Pro	ATG Met	ACC Thr	GAT Asp	GCC Ala	TTC Phe	GAT Asp	GCC Ala	ATG Met	CTT Leu	2294
			685					690					695			
CAA Gln	GCC Ala	GGC Gly	AAC Asn	ATT Ile	GTC Val	TTC Phe	ACC Thr	GTG Val	TTT Phe	TTC Phe	ACA Thr	ATG Met	GAG Glu	ATG Met	GCC Ala	2342
		700					705					710				
TTC Phe	AAG Lys	ATC Ile	ATT Ile	GCC Ala	TTC Phe	GAC Asp	CCC Pro	TAC Tyr	TAT Tyr	TAC Tyr	TTC Phe	CAG Gln	AAG Lys	AAG Lys	TGG Trp	2390
	715					720					725					

AAT Asn 730	ATC Ile	TTC Phe	GAC Asp	TGT Cys	GTC Val 735	ATC Ile	GTC Val	ACC Thr	GTG Val	AGC Ser 740	CTT Leu	CTG Leu	GAG Glu	CTG Leu	AGT Ser 745	2438
GCA Ala	TCC Ser	AAG Lys	AAG Lys	GGC Gly 750	AGC Ser	CTG Leu	TCT Ser	GTG Val	CTC Leu 755	CGT Arg	TCC Ser	TTA Leu	CGC Arg	TTG Leu 760	GCA Ala	2486
CTC Leu	GAC Asp	ACT Thr	ACA Thr 765	GGG Gly	CAG Gln	AAG Lys	AGC Ser	TTC Phe 770	CTG Leu	TCT Ser	GCG Ala	GGC Gly	TAC Tyr 775	TTG Leu	AAC Asn	2534
GAA Glu	CCT Pro	TTC Phe 780	CGA Arg	GCA Ala	CAG Gln	AGG Arg	GCC Ala 785	ATG Met	AGC Ser	GTT Val	GTC Val	AGT Ser 790	ATC Ile	ATG Met	ACT Thr	2582
TCT Ser 795	GTC Val	ATT Ile	GAG Glu	GAG Glu	CTT Leu	GAA Glu 800	GAG Glu	TCT Ser	AAG Lys	CTG Leu	AAG Lys 805	TGC Cys	CCA Pro	CCC Pro	TGC Cys	2630
TTG Leu 810	ATC Ile	AGC Ser	TTC Phe	GCT Ala	CAG Gln 815	AAG Lys	TAT Tyr	CTG Leu	ATC Ile	TGG Trp 820	GAG Glu	TGC Cys	TGC Cys	CCC Pro	AAG Lys 825	2678
TGG Trp	AGG Arg	AAG Lys	TTC Phe	AAG Lys 830	ATG Met	GCG Ala	CTG Leu	TTC Phe	GAG Glu 835	CTG Leu	GTG Val	ACT Thr	GAC Asp	CCC Pro 840	TTC Phe	2726
GCA Ala	GAG Glu	CTT Leu	ACC Thr 845	ATC Ile	ACC Thr	CTC Leu	TGC Cys	ATC Ile 850	GTG Val	GTG Val	AAC Asn	ACC Thr	GTC Val 855	TTC Phe	ATG Met	2774
GCC Ala	ATG Met	GAG Glu 860	CAC His	TAC Tyr	CCC Pro	ATG Met	ACC Thr 865	GAT Asp	GCC Ala	TTC Phe	GAT Asp	GCC Ala 870	ATG Met	CTT Leu	CAA Gln	2822
GCC Ala 875	GGC Gly	AAC Asn	ATT Ile	GTC Val	TTC Phe 880	ACC Thr	GTG Val	TTT Phe	TTC Phe	ACA Thr	ATG Met 885	GAG Glu	ATG Met	GCC Ala	TTC Phe	2870
AAG Lys 890	ATC Ile	ATT Ile	GCC Ala	TTC Phe	GAC Asp 895	CCC Pro	TAC Tyr	TAT Tyr	TAC Tyr	TTC Phe 900	CAG Gln	AAG Lys	AAG Lys	TGG Trp	AAT Asn 905	2918
ATC Ile	TTC Phe	GAC Asp	TGT Cys	GTC Val	ATC Ile 910	GTC Val	ACC Thr	GTG Val	AGC Ser 915	CTT Leu	CTG Leu	GAG Glu	CTG Leu	AGT Ser 920	GCA Ala	2966
TCC Ser	AAG Lys	AAG Lys	GGC Gly 925	AGC Ser	CTG Leu	TCT Ser	GTG Val	CTC Leu	CGT Arg 930	TCC Ser	TTA Leu	CGC Arg	TTG Leu 935	CTG Leu	CGG Arg	3014
GTC Val	TTC Phe	AAG Lys 940	CTG Leu	GCC Ala	AAG Lys	TCC Ser	TGG Trp 945	CCC Pro	ACC Thr	CTG Leu	AAC Asn	ACC Thr 950	CTC Leu	ATC Ile	AAG Lys	3062
ATC Ile 955	ATC Ile	GGG Gly	AAC Asn	TCA Ser	GTG Val	GGG Gly 960	GCC Ala	CTG Leu	GGC Gly	AAC Asn 965	CTG Leu	ACC Thr	TTT Phe	ATC Ile	CTG Leu	3110
GCC Ala 970	ATC Ile	ATC Ile	GTC Val	TTC Phe	ATC Ile 975	TTC Phe	GCC Ala	CTG Leu	GTC Val	GGA Gly 980	AAG Lys	CAG Gln	CTT Leu	CTC Leu	TCA Ser 985	3158

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GAG GAC TAC GGG TGC CGC AAG GAC GGC GTC TCC GTG TGG AAC GGC GAG	3206
Glu Asp Tyr Gly Cys Arg Lys Asp Gly Val Ser Val Trp Asn Gly Glu	
990 1000	
AAG CTC CGC TGG CAC ATG TGT GAC TTC TTC CAT TCC TTC CTG GTC GTC	3254
Lys Leu Arg Trp His Met Cys Asp Phe Phe His Ser Phe Leu Val Val	
1005 1010 1015	
TTC CGA ATC CTC TGC GGG GAG TGG ATC GAG AAC ATG TGG GTC TGC ATG	3302
Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Val Cys Met	
1020 1025 1030	
GAG GTC AGC CAG AAA TCC ATC TGC CTC ATC CTC TTC TTG ACT GTG ATG	3350
Glu Val Ser Gln Lys Ser Ile Cys Leu Ile Leu Phe Leu Thr Val Met	
1035 1040 1045	
GTG CTG GGC AAC CTA GTG GTG CTC AAC CTT TTC ATC GCT TTA CTG CTG	3398
Val Leu Gly Asn Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu	
1050 1055 1060 1065	
AAC TCC TTC AGC GCG GAC AAC CTC ACG GCT CCA GAG GAT GAC GGG GAG	3446
Asn Ser Phe Ser Ala Asp Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu	
1070 1075 1080	
GTG AAC AAC TTG CAG TTA GCA CTG GCC AGG ATC CAG GTA CTT GGC CAT	3494
Val Asn Asn Leu Gln Leu Ala Leu Ala Arg Ile Gln Val Leu Gly His	
1085 1090 1095	
CGG GCC AGC AGG GCC ATC GCC AGT TAC ATC AGC AGC CAC TGC CGA TTC	3542
Arg Ala Ser Arg Ala Ile Ala Ser Tyr Ile Ser Ser His Cys Arg Phe	
1100 1105 1110	
CGC TGG CCC AAG GTG GAG ACC CAG CTG GGC ATG AAG CCC CCA CTC ACC	3590
Arg Trp Pro Lys Val Glu Thr Gln Leu Gly Met Lys Pro Pro Leu Thr	
1115 1120 1125	
AGC TCA GAG GCC AAG AAC CAC ATT GCC ACT GAT GCT GTC AGT GCT GCA	3638
Ser Ser Glu Ala Lys Asn His Ile Ala Thr Asp Ala Val Ser Ala Ala	
1130 1135 1140 1145	
GTG GGG AAC CTG ACA AAG CCA GCT CTC AGT AGC CCC AAG GAG AAT CAC	3686
Val Gly Asn Leu Thr Lys Pro Ala Leu Ser Ser Pro Lys Glu Asn His	
1150 1155 1160	
GGG GAC TTC ATC ACT GAT CCC AAC GTG TGG GTC TCT GTG CCC ATT GCT	3734
Gly Asp Phe Ile Thr Asp Pro Asn Val Trp Val Ser Val Pro Ile Ala	
1165 1170 1175	
GAG GGG GAA TCT GAC CTC GAC GAG CTC GAG GAA GAT ATG GAG CAG GCT	3782
Glu Gly Glu Ser Asp Leu Asp Glu Leu Glu Glu Asp Met Glu Gln Ala	
1180 1185 1190	
TCG CAG AGC TCC TGG CAG GAA GAG GAC CCC AAG GGA CAG CAG GAG CAG	3830
Ser Gln Ser Ser Trp Gln Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln	
1195 1200 1205	
TTG CCA CAA GTC CAA AAG TGT GAA AAC CAC CAG GCA GCC AGA AGC CCA	3878
Leu Pro Gln Val Gln Lys Cys Glu Asn His Gln Ala Ala Arg Ser Pro	
1210 1215 1220 1225	
GCC TCC ATG ATG TCC TCT GAG GAC CTG GCT CCA TAC CTG GGT GAG AGC	3926
Ala Ser Met Met Ser Ser Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser	
1230 1235 1240	

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TGG	AAG	AGG	AAG	GAT	AGC	CCT	CAG	GTC	CCT	GCC	GAG	GGA	GTG	GAT	GAC	3974
Trp	Lys	Arg	Lys	Asp	Ser	Pro	Gln	Val	Pro	Ala	Glu	Gly	Val	Asp	Asp	
			1245					1250					1255			
ACG	AGC	TCC	TCT	GAG	GGC	AGC	ACG	GTG	GAC	TGC	CCG	GAC	CCA	GAG	GAA	4022
Thr	Ser	Ser	Ser	Glu	Gly	Ser	Thr	Val	Asp	Cys	Pro	Asp	Pro	Glu	Glu	
			1260					1265					1270			
ATC	CTG	AGG	AAG	ATC	CCC	GAG	CTG	GCA	GAT	GAC	CTG	GAC	GAG	CCC	GAT	4070
Ile	Leu	Arg	Lys	Ile	Pro	Glu	Leu	Ala	Asp	Asp	Leu	Asp	Glu	Pro	Asp	
			1275				1280					1285				
GAC	TGT	TTC	ACA	GAA	GGC	TGC	ACT	CGC	CGC	TGT	CCC	TGC	TGC	AAC	GTG	4118
Asp	Cys	Phe	Thr	Glu	Gly	Cys	Thr	Arg	Arg	Cys	Pro	Cys	Cys	Asn	Val	
					1295					1300					1305	
AAT	ACT	AGC	AAG	TCT	CCT	TGG	GCC	ACA	GGC	TGG	CAG	GTG	CGC	AAG	ACC	4166
Asn	Thr	Ser	Lys	Ser	Pro	Trp	Ala	Thr	Gly	Trp	Gln	Val	Arg	Lys	Thr	
					1310					1315					1320	
TGC	TAC	CGC	ATC	GTG	GAG	CAC	AGC	TGG	TTT	GAG	AGT	TTC	ATC	ATC	TTC	4214
Cys	Tyr	Arg	Ile	Val	Glu	His	Ser	Trp	Phe	Glu	Ser	Phe	Ile	Ile	Phe	
					1325					1330					1335	
ATG	ATC	CTG	CTC	AGC	AGT	GGA	GCG	CTG	GCC	TTT	GAG	GAT	AAC	TAC	CTG	4262
Met	Ile	Leu	Leu	Ser	Ser	Gly	Ala	Leu	Ala	Phe	Glu	Asp	Asn	Tyr	Leu	
							1345						1350			
GAA	GAG	AAA	CCC	CGA	GTG	AAG	TCC	GTG	CTG	GAG	TAC	ACT	GAC	CGA	GTG	4310
Glu	Glu	Lys	Pro	Arg	Val	Lys	Ser	Val	Leu	Glu	Tyr	Thr	Asp	Arg	Val	
			1355				1360						1365			
TTC	ACC	TTC	ATC	TTC	GTC	TTT	GAG	ATG	CTG	CTC	AAG	TGG	GTA	GCC	TAT	4358
Phe	Thr	Phe	Ile	Phe	Val	Phe	Glu	Met	Leu	Leu	Lys	Trp	Val	Ala	Tyr	
					1375						1380				1385	
GGC	TTC	AAA	AAG	TAT	TTC	ACC	AAT	GCC	TGG	TGC	TGG	CTG	GAC	TTC	CTC	4406
Gly	Phe	Lys	Lys	Tyr	Phe	Thr	Asn	Ala	Trp	Cys	Trp	Leu	Asp	Phe	Leu	
					1390					1395					1400	
ATT	GTG	AAC	ATC	TCC	CTG	ACA	AGC	CTC	ATA	GCG	AAG	ATC	CTT	GAG	TAT	4454
Ile	Val	Asn	Ile	Ser	Leu	Thr	Ser	Leu	Ile	Ala	Lys	Ile	Leu	Glu	Tyr	
					1405				1410					1415		
TCC	GAC	GTG	GCG	TCC	ATC	AAA	GCC	CTT	CGG	ACT	CTC	CGT	GCC	CTC	CGA	4502
Ser	Asp	Val	Ala	Ser	Ile	Lys	Ala	Leu	Arg	Thr	Leu	Arg	Ala	Leu	Arg	
							1425						1430			
CCG	CTG	CGG	GCT	CTG	TCT	CGA	TTC	GAA	GGC	ATG	AGG	GTA	GTG	GTG	GAT	4550
Pro	Leu	Arg	Ala	Leu	Ser	Arg	Phe	Glu	Gly	Met	Arg	Val	Val	Val	Asp	
							1440					1445				
GCC	CTC	GTG	GGC	GCC	ATC	CCC	TCC	ATC	ATG	AAC	GTC	CTC	CTC	GTC	TGC	4598
Ala	Leu	Val	Gly	Ala	Ile	Pro	Ser	Ile	Met	Asn	Val	Leu	Leu	Val	Cys	
						1455					1460				1465	
CTC	ATC	TTC	TGG	CTC	ATC	TTC	AGC	ATC	ATG	GGC	GTG	AAC	CTC	TTC	GCC	4646
Leu	Ile	Phe	Trp	Leu	Ile	Phe	Ser	Ile	Met	Gly	Val	Asn	Leu	Phe	Ala	
						1470				1475					1480	
GGG	AAA	TTT	TCG	AAG	TGC	GTC	GAC	ACC	AGA	AAT	AAC	CCA	TTT	TCC	AAC	4694
Gly	Lys	Phe	Ser	Lys	Cys	Val	Asp	Thr	Arg	Asn	Asn	Pro	Phe	Ser	Asn	
					1485				1490						1495	

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GTG AAT TCG ACG ATG GTG AAT AAC AAG TCC GAG TGT CAC AAT CAA AAC	4742
Val Asn Ser Thr Met Val Asn Asn Lys Ser Glu Cys His Asn Gln Asn	
1500 1505 1510	
AGC ACC GGC CAC TTC TTC TGG GTC AAC GTC AAA GTC AAC TTC GAC AAC	4790
Ser Thr Gly His Phe Phe Trp Val Asn Val Lys Val Asn Phe Asp Asn	
1515 1520 1525	
GTC GCT ATG GGC TAC CTC GCA CTT CTT CAG GTG GCA ACC TTC AAA GGC	4838
Val Ala Met Gly Tyr Leu Ala Leu Leu Gln Val Ala Thr Phe Lys Gly	
1530 1535 1540 1545	
TGG ATG GAC ATA ATG TAT GCA GCT GTT GAT TCC GGA GAG ATC AAC AGT	4886
Trp Met Asp Ile Met Tyr Ala Ala Val Asp Ser Gly Glu Ile Asn Ser	
1550 1555 1560	
CAG CCT AAC TGG GAG AAC AAC TTG TAC ATG TAC CTG TAC TTC GTC GTT	4934
Gln Pro Asn Trp Glu Asn Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val	
1565 1570 1575	
TTC ATC ATT TTC GGT GGC TTC TTC ACG CTG AAT CTC TTT GTT GGG GTC	4982
Phe Ile Ile Phe Gly Gly Phe Phe Thr Leu Asn Leu Phe Val Gly Val	
1580 1585 1590	
ATA ATC GAC AAC TTC AAC CAA CAG AAA AAA AAG CTA GGA GGC CAG GAC	5030
Ile Ile Asp Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp	
1595 1600 1605	
ATC TTC ATG ACA GAA GAG CAG AAG AAG TAC TAC AAT GCC ATG AAG AAG	5078
Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys	
1610 1615 1620 1625	
CTG GGC TCC AAG AAA CCC CAG AAG CCC ATC CCA CGG CCC CTG AAT AAG	5126
Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys	
1630 1635 1640	
TAC CAA GGC TTC GTG TTT GAC ATC GTG ACC AGG CAA GCC TTT GAC ATC	5174
Tyr Gln Gly Phe Val Phe Asp Ile Val Thr Arg Gln Ala Phe Asp Ile	
1645 1650 1655	
ATC ATC ATG GTT CTC ATC TGC CTC AAC ATG ATC ACC ATG ATG GTG GAG	5222
Ile Ile Met Val Leu Ile Cys Leu Asn Met Ile Thr Met Met Val Glu	
1660 1665 1670	
ACC GAC GAG CAG GGC GAG GAG AAG ACG AAG GTT CTG GGC AGA ATC AAC	5270
Thr Asp Glu Gln Gly Glu Glu Lys Thr Lys Val Leu Gly Arg Ile Asn	
1675 1680 1685	
CAG TTC TTT GTG GCC GTC TTC ACG GGC GAG TGT GTG ATG AAG ATG TTC	5318
Gln Phe Phe Val Ala Val Phe Thr Gly Glu Cys Val Met Lys Met Phe	
1690 1695 1700 1705	
GCC CTG CGA CAG TAC TAC TTC ACC AAC GGC TGG AAC GTG TTC GAC TTC	5366
Ala Leu Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp Phe	
1710 1715 1720	
ATA GTG GTG ATC CTG TCC ATT GGG AGT CTG CTG TTT TCT GCA ATC CTT	5414
Ile Val Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu	
1725 1730 1735	
AAG TCA CTG GAA AAC TAC TTC TCC CCG ACG CTC TTC CGG GTC ATC CGT	5462
Lys Ser Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile Arg	
1740 1745 1750	

CTG GCC AGG ATC GGC CGC ATC CTC AGG CTG ATC CGA GCA GCC AAG GGG Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly 1755 1760 1765	5510
ATT CGC ACG CTG CTC TTC GCC CTC ATG ATG TCC CTG CCC GCC CTC TTC Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu Phe 1770 1775 1780 1785	5558
AAC ATC GGC CTC CTC CTC TTC CTC GTC ATG TTC ATC TAC TCC ATC TTC Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile Phe 1790 1795 1800	5606
GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC GGC ATC GAC GAC Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp Asp 1805 1810 1815	5654
ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG TGC CTG TTC CAG Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe Gln 1820 1825 1830	5702
ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC CCC ATC CTC AAC Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn 1835 1840 1845	5750
ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC AGC AAC GGC TCC Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser 1850 1855 1860 1865	5798
CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC TTC TTC ACC ACC Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr Thr 1870 1875 1880	5846
TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATC GCA GTG Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val 1885 1890 1895	5894
ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC ACG GAG CCC CTG Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro Leu 1900 1905 1910	5942
AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG GAG AAG TTC GAC Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp 1915 1920 1925	5990
CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC TCA GAC TTC GCG Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala 1930 1935 1940 1945	6038
GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC AAC CAG AAT ATA Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile 1950 1955 1960	6086
TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT AAG ATC CAC TGT Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His Cys 1965 1970 1975	6134
CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG GGA GAA TCC GGG Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser Gly 1980 1985 1990	6182
GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG TTT ATG GCG ACC Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala Thr 1995 2000 2005	6230

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AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG TGG Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Leu Arg Trp 2010 2015 2020 2025	6278
AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG AGC Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser 2030 2035 2040	6326
TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG CCC Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val Pro 2045 2050 2055	6374
AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC AGT ACA Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ser Thr 2060 2065 2070	6422
TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT GCT Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala 2075 2080 2085	6470
ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT GAC Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp 2090 2095 2100 2105	6518
CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG GTC Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu Val 2110 2115 2120	6566
GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT CAGGCATGCA Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln 2125 2130	6619
CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG AGGTGGCACC	6679
AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA ATGGGGACAT	6739
CCTTGAGAAA GCCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT CCATTCTGAC	6799
GTCCCTTCCG AGTTCCCAGA AGATGTCATT GCTCCCTTCT GTTTGTGACC AGAGACGTGA	6859
TTACCAAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG TGTCGGGCAG	6919
TCTTAGAGAA GTCACGTAGG GGTTGGTACT GAGAATTAGG GTTTGCATGA CTGCATGCTC	6979
ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTTA AAGTTAAAAA	7039
AAAAAAAAAA AAA	7052

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Leu	Pro	Phe	Ala	Ser	Val	Gly	Thr	Thr	Asn	Phe	Arg	Arg	Phe
1				5				10						15	

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Thr Pro Glu Ser Leu Ala Glu Ile Glu Lys Gln Ile Ala Ala His Arg
 20 25 30
 Ala Ala Lys Lys Ala Arg Thr Lys His Arg Gly Gln Glu Asp Lys Gly
 35 40 45
 Glu Lys Pro Arg Pro Gln Leu Asp Leu Lys Asp Cys Asn Gln Leu Pro
 50 55 60
 Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
 65 70 75 80
 Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
 85 90 95
 Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
 100 105 110
 Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
 115 120 125
 His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
 130 135 140
 Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
 145 150 155 160
 Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
 165 170 175
 Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
 180 185 190
 Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
 195 200 205
 Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
 210 215 220
 Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
 225 230 235 240
 His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
 245 250 255
 Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
 260 265 270
 Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
 275 280 285
 Leu Ser Ser Glu Met Ala Glu Tyr Ile Phe Ile Lys Pro Gly Thr Thr
 290 295 300
 Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320
 Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 325 330 335
 Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350

Thr	Gln	Asp	Ser	Trp	Glu	Arg	Leu	Tyr	Gln	Gln	Thr	Leu	Arg	Ala	Ser
		355					360					365			
Gly	Lys	Met	Tyr	Met	Val	Phe	Phe	Val	Leu	Val	Ile	Phe	Leu	Gly	Ser
	370					375					380				
Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	Val	Val	Thr	Met	Ala	Tyr	Glu
385					390					395					400
Glu	Gln	Ser	Gln	Ala	Thr	Ile	Ala	Glu	Ile	Glu	Ala	Lys	Glu	Lys	Lys
				405					410					415	
Phe	Gln	Glu	Ala	Leu	Glu	Val	Leu	Gln	Lys	Glu	Gln	Glu	Val	Leu	Ala
			420					425					430		
Ala	Leu	Gly	Ile	Asp	Thr	Thr	Ser	Leu	Gln	Ser	His	Ser	Gly	Ser	Pro
		435					440					445			
Leu	Ala	Ser	Lys	Asn	Ala	Asn	Glu	Arg	Arg	Pro	Arg	Val	Lys	Ser	Arg
	450					455					460				
Val	Ser	Glu	Gly	Ser	Thr	Asp	Asp	Asn	Arg	Ser	Pro	Gln	Ser	Asp	Pro
465					470					475					480
Tyr	Asn	Gln	Arg	Arg	Met	Ser	Phe	Leu	Gly	Leu	Ser	Ser	Gly	Arg	Arg
				485					490					495	
Arg	Ala	Ser	His	Gly	Ser	Val	Phe	His	Phe	Arg	Ala	Pro	Ser	Gln	Asp
			500					505					510		
Ile	Ser	Phe	Pro	Asp	Gly	Ile	Thr	Pro	Asp	Asp	Gly	Val	Phe	His	Gly
		515					520					525			
Asp	Gln	Glu	Ser	Arg	Arg	Gly	Ser	Ile	Leu	Leu	Gly	Arg	Gly	Ala	Gly
	530					535					540				
Gln	Thr	Gly	Pro	Leu	Pro	Arg	Ser	Pro	Leu	Pro	Gln	Ser	Pro	Asn	Pro
545					550					555					560
Gly	Arg	Arg	His	Gly	Glu	Glu	Gly	Gln	Leu	Gly	Val	Pro	Thr	Gly	Glu
				565					570					575	
Leu	Thr	Ala	Gly	Ala	Pro	Glu	Gly	Pro	Ala	Leu	Asp	Thr	Thr	Gly	Gln
			580					585					590		
Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	Asn	Glu	Pro	Phe	Arg	Ala	Gln
		595					600					605			
Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	Thr	Ser	Val	Ile	Glu	Glu	Leu
		610				615					620				
Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	Cys	Leu	Ile	Ser	Phe	Ala	Gln
625					630					635					640
Lys	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	Lys	Trp	Arg	Lys	Phe	Lys	Met
				645					650					655	
Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	Phe	Ala	Glu	Leu	Thr	Ile	Thr
			660					665					670		
Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	Met	Ala	Met	Glu	His	Tyr	Pro
		675					680					685			

81

Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	Gln	Ala	Gly	Asn	Ile	Val	Phe
690						695					700				
Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	Phe	Lys	Ile	Ile	Ala	Phe	Asp
705					710					715					720
Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	Asn	Ile	Phe	Asp	Cys	Val	Ile
				725					730					735	
Val	Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	Ala	Ser	Lys	Lys	Gly	Ser	Leu
			740					745					750		
Ser	Val	Leu	Arg	Ser	Leu	Arg	Leu	Ala	Leu	Asp	Thr	Thr	Gly	Gln	Lys
		755					760					765			
Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	Asn	Glu	Pro	Phe	Arg	Ala	Gln	Arg
	770					775					780				
Ala	Met	Ser	Val	Val	Ser	Ile	Met	Thr	Ser	Val	Ile	Glu	Glu	Leu	Glu
785					790					795					800
Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	Cys	Leu	Ile	Ser	Phe	Ala	Gln	Lys
				805					810					815	
Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	Lys	Trp	Arg	Lys	Phe	Lys	Met	Ala
			820					825					830		
Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	Phe	Ala	Glu	Leu	Thr	Ile	Thr	Leu
		835					840					845			
Cys	Ile	Val	Val	Asn	Thr	Val	Phe	Met	Ala	Met	Glu	His	Tyr	Pro	Met
	850					855					860				
Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	Gln	Ala	Gly	Asn	Ile	Val	Phe	Thr
865					870					875					880
Val	Phe	Phe	Thr	Met	Glu	Met	Ala	Phe	Lys	Ile	Ile	Ala	Phe	Asp	Pro
				885					890					895	
Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	Asn	Ile	Phe	Asp	Cys	Val	Ile	Val
			900					905					910		
Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	Ala	Ser	Lys	Lys	Gly	Ser	Leu	Ser
		915					920					925			
Val	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser
	930					935					940				
Trp	Pro	Thr	Leu	Asn	Thr	Leu	Ile	Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly
945					950					955					960
Ala	Leu	Gly	Asn	Leu	Thr	Phe	Ile	Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe
				965					970					975	
Ala	Leu	Val	Gly	Lys	Gln	Leu	Leu	Ser	Glu	Asp	Tyr	Gly	Cys	Arg	Lys
			980					985					990		
Asp	Gly	Val	Ser	Val	Trp	Asn	Gly	Glu	Lys	Leu	Arg	Trp	His	Met	Cys
		995					1000					1005			
Asp	Phe	Phe	His	Ser	Phe	Leu	Val	Val	Phe	Arg	Ile	Leu	Cys	Gly	Glu
	1010					1015					1020				

82

Trp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser Ile
 1025 1030 1035 1040
 Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val Val
 1045 1050 1055
 Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Ala Asp Asn
 1060 1065 1070
 Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu Ala
 1075 1080 1085
 Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ile Ala
 1090 1095 1100
 Ser Tyr Ile Ser Ser His Cys Arg Phe Arg Trp Pro Lys Val Glu Thr
 1105 1110 1115 1120
 Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn His
 1125 1130 1135
 Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys Pro
 1140 1145 1150
 Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp Pro
 1155 1160 1165
 Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu Asp
 1170 1175 1180
 Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln Glu
 1185 1190 1195 1200
 Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys Cys
 1205 1210 1215
 Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser Glu
 1220 1225 1230
 Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser Pro
 1235 1240 1245
 Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly Ser
 1250 1255 1260
 Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro Glu
 1265 1270 1275 1280
 Leu Ala Asp Asp Leu Asp Glu Pro Asp Asp Cys Phe Thr Glu Gly Cys
 1285 1290 1295
 Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro Trp
 1300 1305 1310
 Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu His
 1315 1320 1325
 Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser Gly
 1330 1335 1340
 Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val Lys
 1345 1350 1355 1360
 Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val Phe
 1365 1370 1375

83

Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe Thr
1380 1385 1390

Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu Thr
1395 1400 1405

Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile Lys
1410 1415 1420

Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg
1425 1430 1435 1440

Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile Pro
1445 1450 1455

Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe
1460 1465 1470

Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys Val
1475 1480 1485

Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val Asn
1490 1495 1500

Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe Trp
1505 1510 1515 1520

Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu Ala
1525 1530 1535

Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr Ala
1540 1545 1550

Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn Asn
1555 1560 1565

Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly Phe
1570 1575 1580

Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn Gln
1585 1590 1595 1600

Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu Gln
1605 1610 1615

Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro Gln
1620 1625 1630

Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe Asp
1635 1640 1645

Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile Cys
1650 1655 1660

Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu Glu
1665 1670 1675 1680

Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val Phe
1685 1690 1695

Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr Phe
1700 1705 1710

84

Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser Ile
1715 1720 1725

Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr Phe
1730 1735 1740

Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile
1745 1750 1755 1760

Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala
1765 1770 1775

Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
1780 1785 1790

Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala Asn
1795 1800 1805

Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr Phe
1810 1815 1820

Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp
1825 1830 1835 1840

Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys Asp
1845 1850 1855

Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser Pro
1860 1865 1870

Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe Leu
1875 1880 1885

Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn Val
1890 1895 1900

Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp Met
1905 1910 1915 1920

Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe Ile
1925 1930 1935

Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro Leu
1940 1945 1950

Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu Pro
1955 1960 1965

Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala Phe
1970 1975 1980

Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys Thr
1985 1990 1995 2000

Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser Tyr
2005 2010 2015

Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser Ala
2020 2025 2030

Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser Leu
2035 2040 2045

85

Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly Val
 2050 2055 2060
 Ser Leu Pro Gly Glu Gly Tyr Ser Thr Phe Met Ala Asn Ser Gly Leu
 2065 2070 2075 2080
 Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser Tyr
 2085 2090 2095
 Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro Ser
 2100 2105 2110
 Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn Ser
 2115 2120 2125
 Pro Gly Pro Gln
 2130

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 204..6077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TAGCTTGCTT CTGCTAATGC TACCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG	60
TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTTTC	120
AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAAA GAGTGTAAT	180
TCTTCCCCAA GAAGAATGAG AAG ATG GAG CTC CCC TTT GCG TCC GTG GGA	230
Met Glu Leu Pro Phe Ala Ser Val Gly	
1 5	
ACT ACC AAT TTC AGA CGG TTC ACT CCA GAG TCA CTG GCA GAG ATC GAG	278
Thr Thr Asn Phe Arg Arg Phe Thr Pro Glu Ser Leu Ala Glu Ile Glu	
10 15 20 25	
AAG CAG ATT GCT GCT CAC CGG GCA GCC AAG AAG GCC AGA ACC AAG CAC	326
Lys Gln Ile Ala Ala His Arg Ala Ala Lys Lys Ala Arg Thr Lys His	
30 35 40	
AGA GGA CAG GAG GAC AAG GGC GAG AAG CCC AGG CCT CAG CTG GAC TTG	374
Arg Gly Gln Glu Asp Lys Gly Glu Lys Pro Arg Pro Gln Leu Asp Leu	
45 50 55	
AAA GAC TGT AAC CAG CTG CCC AAG TTC TAT GGT GAG CTC CCA GCA GAA	422
Lys Asp Cys Asn Gln Leu Pro Lys Phe Tyr Gly Glu Leu Pro Ala Glu	
60 65 70	

86

CTG Leu	GTC Val 75	GGG Gly	GAG Glu	CCC Pro	CTG Leu	GAG Glu 80	GAC Asp	CTA Leu	GAC Asp	CCT Pro	TTC Phe 85	TAC Tyr	AGC Ser	ACA Thr	CAC His	470
CGG Arg 90	ACA Thr	TTC Phe	ATG Met	GTG Val	TTG Leu 95	AAT Asn	AAA Lys	AGC Ser	AGG Arg	ACC Thr 100	ATT Ile	TCC Ser	AGA Arg	TTC Phe	AGT Ser 105	518
GCC Ala	ACT Thr	TGG Trp	GCC Ala	CTG Leu 110	TGG Trp	CTC Leu	TTC Phe	AGT Ser	CCC Pro 115	TTC Phe	AAC Asn	CTG Leu	ATC Ile	AGA Arg 120	AGA Arg	566
ACA Thr	GCC Ala	ATC Ile	AAA Lys 125	GTG Val	TCT Ser	GTC Val	CAT His	TCC Ser 130	TGG Trp	TTC Phe	TCC Ser	ATA Ile	TTC Phe 135	ATC Ile	ACC Thr	614
ATC Ile	ACT Thr 140	ATT Ile	TTG Leu	GTC Val	AAC Asn	TGC Cys	GTG Val 145	TGC Cys	ATG Met	ACC Thr	CGA Arg	ACT Thr 150	GAT Asp	CTT Leu	CCA Pro	662
GAG Glu 155	AAA Lys	GTC Val	GAG Glu	TAC Tyr	GTC Val	TTC Phe 160	ACT Thr	GTC Val	ATT Ile	TAC Tyr	ACC Thr 165	TTC Phe	GAG Glu	GCT Ala	CTG Leu	710
ATT Ile 170	AAG Lys	ATA Ile	CTG Leu	GCA Ala	AGA Arg 175	GGG Gly	TTT Phe	TGT Cys	CTA Leu	AAT Asn 180	GAG Glu	TTC Phe	ACT Thr	TAT Tyr	CTT Leu 185	758
CGA Arg	GAT Asp	CCG Pro	TGG Trp	AAC Asn 190	TGG Trp	CTG Leu	GAC Asp	TTC Phe	AGT Ser 195	GTC Val	ATT Ile	ACC Thr	TTG Leu	GCG Ala 200	TAT Tyr	806
GTG Val	GGT Gly	GCA Ala 205	GCG Ala	ATA Ile	GAC Asp	CTC Leu	CGA Arg	GGA Gly 210	ATC Ile	TCA Ser	GGC Gly	CTG Leu 215	CGG Arg	ACA Thr	TTC Phe	854
CGA Arg	GTT Val 220	CTC Leu	AGA Arg	GCC Ala	CTG Leu	AAA Lys	ACT Thr 225	GTT Val	TCT Ser	GTG Val	ATC Ile	CCA Pro 230	GGA Gly	CTG Leu	AAG Lys	902
GTC Val 235	ATC Ile	GTG Val	GGA Gly	GCC Ala	CTG Leu	ATC Ile 240	CAC His	TCA Ser	GTG Val	AGG Arg	AAG Lys 245	CTG Leu	GCC Ala	GAC Asp	GTG Val	950
ACT Thr 250	ATC Ile	CTC Leu	ACA Thr	GTC Val	TTC Phe 255	TGC Cys	CTG Leu	AGC Ser	GTC Val	TTC Phe 260	GCC Ala	TTG Leu	GTG Val	GGC Gly	CTG Leu 265	998
CAG Gln	CTC Leu	TTT Phe	AAG Lys	GGG Gly 270	AAC Asn	CTT Leu	AAG Lys	AAC Asn	AAA Lys 275	TGC Cys	ATC Ile	AGG Arg	AAC Asn	GGA Gly 280	ACA Thr	1046
GAT Asp	CCC Pro	CAC His	AAG Lys 285	GCT Ala	GAC Asp	AAC Asn	CTC Leu	TCA Ser	TCT Ser	GAA Glu	ATG Met	GCA Ala	GAA Glu 295	TAC Tyr	ATC Ile	1094
TTC Phe	ATC Ile	AAG Lys 300	CCT Pro	GGT Gly	ACT Thr	ACG Thr	GAT Asp 305	CCC Pro	TTA Leu	CTG Leu	TGC Cys	GGC Gly 310	AAT Asn	GGG Gly	TCT Ser	1142
GAT Asp	GCT Ala 315	GGT Gly	CAC His	TGC Cys	CCT Pro	GGA Gly 320	GGC Gly	TAT Tyr	GTC Val	TGC Cys	CTG Leu 325	AAA Lys	ACT Thr	CCT Pro	GAC Asp	1190

AAC Asn 330	CCG Pro	GAT Asp	TTT Phe	AAC Asn	TAC Tyr 335	ACC Thr	AGC Ser	TTT Phe	GAT Asp	TCC Ser 340	TTT Phe	GCG Ala	TGG Trp	GCA Ala	TTC Phe 345	1238
CTC Leu	TCA Ser	CTG Leu	TTC Phe	CGC Arg 350	CTC Leu	ATG Met	ACG Thr	CAG Gln	GAC Asp 355	TCC Ser	TGG Trp	GAG Glu	CGC Arg	CTG Leu 360	TAC Tyr	1286
CAG Gln	CAG Gln	ACA Thr	CTC Leu 365	CGG Arg	GCT Ala	TCT Ser	GGG Gly	AAA Lys 370	ATG Met	TAC Tyr	ATG Met	GTC Val	TTT Phe 375	TTC Phe	GTG Val	1334
CTG Leu	GTT Val	ATT Ile 380	TTC Phe	CTT Leu	GGA Gly	TCG Ser	TTC Phe 385	TAC Tyr	CTG Leu	GTC Val	AAT Asn	TTG Leu 390	ATC Ile	TTG Leu	GCC Ala	1382
GTG Val 395	GTC Val	ACC Thr	ATG Met	GCG Ala	TAT Tyr	GAA Glu 400	GAG Glu	CAG Gln	AGC Ser	CAG Gln	GCA Ala 405	ACA Thr	ATT Ile	GCA Ala	GAA Glu	1430
ATC Ile 410	GAA Glu	GCC Ala	AAG Lys	GAA Glu	AAA Lys 415	AAG Lys	TTC Phe	CAG Gln	GAA Glu	GCC Ala 420	CTT Leu	GAG Glu	GTG Val	CTG Leu	CAG Gln 425	1478
AAG Lys	GAA Glu	CAG Gln	GAG Glu	GTG Val 430	CTG Leu	GCA Ala	GCC Ala	CTG Leu	GGG Gly 435	ATT Ile	GAC Asp	ACG Thr	ACC Thr	TCG Ser 440	CTC Leu	1526
CAG Gln	TCC Ser	CAC His	AGT Ser 445	GGA Gly	TCA Ser	CCC Pro	TTA Leu 450	GCC Ala	TCC Ser	AAA Lys	AAC Asn	GCC Ala	AAT Asn 455	GAG Glu	AGA Arg	1574
AGA Arg	CCC Pro	AGG Arg 460	GTG Val	AAA Lys	TCA Ser	AGG Arg	GTG Val 465	TCA Ser	GAG Glu	GGC Gly	TCC Ser	ACG Thr 470	GAT Asp	GAC Asp	AAC Asn	1622
AGG Arg 475	TCA Ser	CCC Pro	CAA Gln	TCT Ser	GAC Asp 480	CCT Pro	TAC Tyr	AAC Asn	CAG Gln	CGC Arg	AGG Arg 485	ATG Met	TCT Ser	TTC Phe	CTA Leu	1670
GGC Gly 490	CTG Leu	TCT Ser	TCA Ser	GGA Gly	AGA Arg 495	CGC Arg	AGG Arg	GCT Ala	AGC Ser	CAC His 500	GGC Gly	AGT Ser	GTG Val	TTC Phe	CAC His 505	1718
TTC Phe	CGA Arg	GCG Ala	CCC Pro	AGC Ser 510	CAA Gln	GAC Asp	ATC Ile	TCA Ser	TTT Phe 515	CCT Pro	GAC Asp	GGG Gly	ATC Ile	ACC Thr 520	CCT Pro	1766
GAT Asp	GAT Asp	GGG Gly	GTC Val 525	TTT Phe	CAC His	GGA Gly	GAC Asp	CAG Gln	GAA Glu	AGC Ser	CGT Arg	CGA Arg	GGT Gly 535	TCC Ser	ATA Ile	1814
TTG Leu	CTG Leu	GGC Gly 540	AGG Arg	GGT Gly	GCT Ala	GGG Gly	CAG Gln	ACA Thr	GGT Gly	CCA Pro	CTC Leu	CCC Pro 550	AGG Arg	AGC Ser	CCA Pro	1862
CTG Leu 555	CCT Pro	CAG Gln	TCC Ser	CCC Pro	AAC Asn	CCT Pro 560	GGC Gly	CGT Arg	AGA Arg	CAT His	GGA Gly 565	GAA Glu	GAG Glu	GGA Gly	CAG Gln	1910
CTC Leu 570	GGA Gly	GTG Val	CCC Pro	ACT Thr	GGT Gly 575	GAG Glu	CTT Leu	ACC Thr	GCT Ala	GGA Gly 580	GCG Ala	CCT Pro	GAA Glu	GGC Gly	CCG Pro 585	1958

GCA	CTC	GAC	ACT	ACA	GGG	CAG	AAG	AGC	TTC	CTG	TCT	GCG	GGC	TAC	TTG	2006
Ala	Leu	Asp	Thr	Thr	Gly	Gln	Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	
				590					595					600		
AAC	GAA	CCT	TTC	CGA	GCA	CAG	AGG	GCC	ATG	AGC	GTT	GTC	AGT	ATC	ATG	2054
Asn	Glu	Pro	Phe	Arg	Ala	Gln	Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	
			605					610					615			
ACT	TCT	GTC	ATT	GAG	GAG	CTT	GAA	GAG	TCT	AAG	CTG	AAG	TGC	CCA	CCC	2102
Thr	Ser	Val	Ile	Glu	Glu	Leu	Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	
		620					625					630				
TGC	TTG	ATC	AGC	TTC	GCT	CAG	AAG	TAT	CTG	ATC	TGG	GAG	TGC	TGC	CCC	2150
Cys	Leu	Ile	Ser	Phe	Ala	Gln	Lys	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	
	635					640					645					
AAG	TGG	AGG	AAG	TTC	AAG	ATG	GCG	CTG	TTC	GAG	CTG	GTG	ACT	GAC	CCC	2198
Lys	Trp	Arg	Lys	Phe	Lys	Met	Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	
	650				655					660					665	
TTC	GCA	GAG	CTT	ACC	ATC	ACC	CTC	TGC	ATC	GTG	GTG	AAC	ACC	GTC	TTC	2246
Phe	Ala	Glu	Leu	Thr	Ile	Thr	Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	
				670					675					680		
ATG	GCC	ATG	GAG	CAC	TAC	CCC	ATG	ACC	GAT	GCC	TTC	GAT	GCC	ATG	CTT	2294
Met	Ala	Met	Glu	His	Tyr	Pro	Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	
			685					690					695			
CAA	GCC	GGC	AAC	ATT	GTC	TTC	ACC	GTG	TTT	TTC	ACA	ATG	GAG	ATG	GCC	2342
Gln	Ala	Gly	Asn	Ile	Val	Phe	Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	
		700					705					710				
TTC	AAG	ATC	ATT	GCC	TTC	GAC	CCC	TAC	TAT	TAC	TTC	CAG	AAG	AAG	TGG	2390
Phe	Lys	Ile	Ile	Ala	Phe	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	
	715					720					725					
AAT	ATC	TTC	GAC	TGT	GTC	ATC	GTC	ACC	GTG	AGC	CTT	CTG	GAG	CTG	AGT	2438
Asn	Ile	Phe	Asp	Cys	Val	Ile	Val	Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	
	730				735					740					745	
GCA	TCC	AAG	AAG	GGC	AGC	CTG	TCT	GTG	CTC	CGT	TCC	TTA	CGC	TTG	CTG	2486
Ala	Ser	Lys	Lys	Gly	Ser	Leu	Ser	Val	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				750					755					760		
CGG	GTC	TTC	AAG	CTG	GCC	AAG	TCC	TGG	CCC	ACC	CTG	AAC	ACC	CTC	ATC	2534
Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	Thr	Leu	Ile	
			765					770					775			
AAG	ATC	ATC	GGG	AAC	TCA	GTG	GGG	GCC	CTG	GGC	AAC	CTG	ACC	TTT	ATC	2582
Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	Asn	Leu	Thr	Phe	Ile	
		780					785					790				
CTG	GCC	ATC	ATC	GTC	TTC	ATC	TTC	GCC	CTG	GTC	GGA	AAG	CAG	CTT	CTC	2630
Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Leu	Val	Gly	Lys	Gln	Leu	Leu	
	795					800					805					
TCA	GAG	GAC	TAC	GGG	TGC	CGC	AAG	GAC	GGC	GTC	TCC	GTG	TGG	AAC	GGC	2678
Ser	Glu	Asp	Tyr	Gly	Cys	Arg	Lys	Asp	Gly	Val	Ser	Val	Trp	Asn	Gly	
	810				815					820					825	
GAG	AAG	CTC	CGC	TGG	CAC	ATG	TGT	GAC	TTC	TTC	CAT	TCC	TTC	CTG	GTC	2726
Glu	Lys	Leu	Arg	Trp	His	Met	Cys	Asp	Phe	Phe	His	Ser	Phe	Leu	Val	
				830					835					840		

89

GTC	TTC	CGA	ATC	CTC	TGC	GGG	GAG	TGG	ATC	GAG	AAC	ATG	TGG	GTC	TGC	2774
Val	Phe	Arg	Ile	Leu	Cys	Gly	Glu	Trp	Ile	Glu	Asn	Met	Trp	Val	Cys	
			845					850					855			
ATG	GAG	GTC	AGC	CAG	AAA	TCC	ATC	TGC	CTC	ATC	CTC	TTC	TTG	ACT	GTG	2822
Met	Glu	Val	Ser	Gln	Lys	Ser	Ile	Cys	Leu	Ile	Leu	Phe	Leu	Thr	Val	
		860					865					870				
ATG	GTG	CTG	GGC	AAC	CTA	GTG	GTG	CTC	AAC	CTT	TTC	ATC	GCT	TTA	CTG	2870
Met	Val	Leu	Gly	Asn	Leu	Val	Val	Leu	Asn	Leu	Phe	Ile	Ala	Leu	Leu	
	875					880					885					
CTG	AAC	TCC	TTC	AGC	GCG	GAC	AAC	CTC	ACG	GCT	CCA	GAG	GAT	GAC	GGG	2918
Leu	Asn	Ser	Phe	Ser	Ala	Asp	Asn	Leu	Thr	Ala	Pro	Glu	Asp	Asp	Gly	
890					895					900					905	
GAG	GTG	AAC	AAC	TTG	CAG	TTA	GCA	CTG	GCC	AGG	ATC	CAG	GTA	CTT	GGC	2966
Glu	Val	Asn	Asn	Leu	Gln	Leu	Ala	Leu	Ala	Arg	Ile	Gln	Val	Leu	Gly	
				910					915					920		
CAT	CGG	GCC	AGC	AGG	GCC	ATC	GCC	AGT	TAC	ATC	AGC	AGC	CAC	TGC	CGA	3014
His	Arg	Ala	Ser	Arg	Ala	Ile	Ala	Ser	Tyr	Ile	Ser	Ser	His	Cys	Arg	
			925					930					935			
TTC	CGC	TGG	CCC	AAG	GTG	GAG	ACC	CAG	CTG	GGC	ATG	AAG	CCC	CCA	CTC	3062
Phe	Arg	Trp	Pro	Lys	Val	Glu	Thr	Gln	Leu	Gly	Met	Lys	Pro	Pro	Leu	
		940					945					950				
ACC	AGC	TCA	GAG	GCC	AAG	AAC	CAC	ATT	GCC	ACT	GAT	GCT	GTC	AGT	GCT	3110
Thr	Ser	Ser	Glu	Ala	Lys	Asn	His	Ile	Ala	Thr	Asp	Ala	Val	Ser	Ala	
	955					960					965					
GCA	GTG	GGG	AAC	CTG	ACA	AAG	CCA	GCT	CTC	AGT	AGC	CCC	AAG	GAG	AAT	3158
Ala	Val	Gly	Asn	Leu	Thr	Lys	Pro	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Asn	
970					975					980					985	
CAC	GGG	GAC	TTC	ATC	ACT	GAT	CCC	AAC	GTG	TGG	GTC	TCT	GTG	CCC	ATT	3206
His	Gly	Asp	Phe	Ile	Thr	Asp	Pro	Asn	Val	Trp	Val	Ser	Val	Pro	Ile	
				990					995					1000		
GCT	GAG	GGG	GAA	TCT	GAC	CTC	GAC	GAG	CTC	GAG	GAA	GAT	ATG	GAG	CAG	3254
Ala	Glu	Gly	Glu	Ser	Asp	Leu	Asp	Glu	Leu	Glu	Glu	Asp	Met	Glu	Gln	
			1005					1010					1015			
GCT	TCG	CAG	AGC	TCC	TGG	CAG	GAA	GAG	GAC	CCC	AAG	GGA	CAG	CAG	GAG	3302
Ala	Ser	Gln	Ser	Ser	Trp	Gln	Glu	Glu	Asp	Pro	Lys	Gly	Gln	Gln	Glu	
		1020					1025					1030				
CAG	TTG	CCA	CAA	GTC	CAA	AAG	TGT	GAA	AAC	CAC	CAG	GCA	GCC	AGA	AGC	3350
Gln	Leu	Pro	Gln	Val	Gln	Lys	Cys	Glu	Asn	His	Gln	Ala	Ala	Arg	Ser	
	1035					1040					1045					
CCA	GCC	TCC	ATG	ATG	TCC	TCT	GAG	GAC	CTG	GCT	CCA	TAC	CTG	GGT	GAG	3398
Pro	Ala	Ser	Met	Met	Ser	Ser	Glu	Asp	Leu	Ala	Pro	Tyr	Leu	Gly	Glu	
1050					1055					1060					1065	
AGC	TGG	AAG	AGG	AAG	GAT	AGC	CCT	CAG	GTC	CCT	GCC	GAG	GGA	GTG	GAT	3446
Ser	Trp	Lys	Arg	Lys	Asp	Ser	Pro	Gln	Val	Pro	Ala	Glu	Gly	Val	Asp	
				1070					1075					1080		
GAC	ACG	AGC	TCC	TCT	GAG	GGC	AGC	ACG	GTG	GAC	TGC	CCG	GAC	CCA	GAG	3494
Asp	Thr	Ser	Ser	Ser	Glu	Gly	Ser	Thr	Val	Asp	Cys	Pro	Asp	Pro	Glu	
			1085					1090					1095			

GAA ATC CTG AGG AAG ATC CCC GAG CTG GCA GAT GAC CTG GAC GAG CCC Glu Ile Leu Arg Lys Ile Pro Glu Leu Ala Asp Asp Leu Asp Glu Pro 1100 1105 1110	3542
GAT GAC TGT TTC ACA GAA GGC TGC ACT CGC CGC TGT CCC TGC TGC AAC Asp Asp Cys Phe Thr Glu Gly Cys Thr Arg Arg Cys Pro Cys Cys Asn 1115 1120 1125	3590
GTG AAT ACT AGC AAG TCT CCT TGG GCC ACA GGC TGG CAG GTG CGC AAG Val Asn Thr Ser Lys Ser Pro Trp Ala Thr Gly Trp Gln Val Arg Lys 1130 1135 1140 1145	3638
ACC TGC TAC CGC ATC GTG GAG CAC AGC TGG TTT GAG AGT TTC ATC ATC Thr Cys Tyr Arg Ile Val Glu His Ser Trp Phe Glu Ser Phe Ile Ile 1150 1155 1160	3686
TTC ATG ATC CTG CTC AGC AGT GGA GCG CTG GCC TTT GAG GAT AAC TAC Phe Met Ile Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Asn Tyr 1165 1170 1175	3734
CTG GAA GAG AAA CCC CGA GTG AAG TCC GTG CTG GAG TAC ACT GAC CGA Leu Glu Glu Lys Pro Arg Val Lys Ser Val Leu Glu Tyr Thr Asp Arg 1180 1185 1190	3782
GTG TTC ACC TTC ATC TTC GTC TTT GAG ATG CTG CTC AAG TGG GTA GCC Val Phe Thr Phe Ile Phe Val Phe Glu Met Leu Leu Lys Trp Val Ala 1195 1200 1205	3830
TAT GGC TTC AAA AAG TAT TTC ACC AAT GCC TGG TGC TGG CTG GAC TTC Tyr Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe 1210 1215 1220 1225	3878
CTC ATT GTG AAC ATC TCC CTG ACA AGC CTC ATA GCG AAG ATC CTT GAG Leu Ile Val Asn Ile Ser Leu Thr Ser Leu Ile Ala Lys Ile Leu Glu 1230 1235 1240	3926
TAT TCC GAC GTG GCG TCC ATC AAA GCC CTT CGG ACT CTC CGT GCC CTC Tyr Ser Asp Val Ala Ser Ile Lys Ala Leu Arg Thr Leu Arg Ala Leu 1245 1250 1255	3974
CGA CCG CTG CGG GCT CTG TCT CGA TTC GAA GGC ATG AGG GTA GTG GTG Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val 1260 1265 1270	4022
GAT GCC CTC GTG GGC GCC ATC CCC TCC ATC ATG AAC GTC CTC CTC GTC Asp Ala Leu Val Gly Ala Ile Pro Ser Ile Met Asn Val Leu Leu Val 1275 1280 1285	4070
TGC CTC ATC TTC TGG CTC ATC TTC AGC ATC ATG GGC GTG AAC CTC TTC Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile Met Gly Val Asn Leu Phe 1290 1295 1300 1305	4118
GCC GGG AAA TTT TCG AAG TGC GTC GAC ACC AGA AAT AAC CCA TTT TCC Ala Gly Lys Phe Ser Lys Cys Val Asp Thr Arg Asn Asn Pro Phe Ser 1310 1315 1320	4166
AAC GTG AAT TCG ACG ATG GTG AAT AAC AAG TCC GAG TGT CAC AAT CAA Asn Val Asn Ser Thr Met Val Asn Asn Lys Ser Glu Cys His Asn Gln 1325 1330 1335	4214
AAC AGC ACC GGC CAC TTC TTC TGG GTC AAC GTC AAA GTC AAC TTC GAC Asn Ser Thr Gly His Phe Phe Trp Val Asn Val Lys Val Asn Phe Asp 1340 1345 1350	4262

AAC GTC GCT ATG GGC TAC CTC GCA CTT CTT CAG GTG GCA ACC TTC AAA Asn Val Ala Met Gly Tyr Leu Ala Leu Leu Gln Val Ala Thr Phe Lys 1355 1360 1365	4310
GGC TGG ATG GAC ATA ATG TAT GCA GCT GTT GAT TCC GGA GAG ATC AAC Gly Trp Met Asp Ile Met Tyr Ala Ala Val Asp Ser Gly Glu Ile Asn 1370 1375 1380 1385	4358
AGT CAG CCT AAC TGG GAG AAC AAC TTG TAC ATG TAC CTG TAC TTC GTC Ser Gln Pro Asn Trp Glu Asn Asn Leu Tyr Met Tyr Leu Tyr Phe Val 1390 1395 1400	4406
GTT TTC ATC ATT TTC GGT GGC TTC TTC ACG CTG AAT CTC TTT GTT GGG Val Phe Ile Ile Phe Gly Gly Phe Phe Thr Leu Asn Leu Phe Val Gly 1405 1410 1415	4454
GTC ATA ATC GAC AAC TTC AAC CAA CAG AAA AAA AAG CTA GGA GGC CAG Val Ile Ile Asp Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Gln 1420 1425 1430	4502
GAC ATC TTC ATG ACA GAA GAG CAG AAG AAG TAC TAC AAT GCC ATG AAG Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys 1435 1440 1445	4550
AAG CTG GGC TCC AAG AAA CCC CAG AAG CCC ATC CCA CGG CCC CTG AAT Lys Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn 1450 1455 1460 1465	4598
AAG TAC CAA GGC TTC GTG TTT GAC ATC GTG ACC AGG CAA GCC TTT GAC Lys Tyr Gln Gly Phe Val Phe Asp Ile Val Thr Arg Gln Ala Phe Asp 1470 1475 1480	4646
ATC ATC ATC ATG GTT CTC ATC TGC CTC AAC ATG ATC ACC ATG ATG GTG Ile Ile Ile Met Val Leu Ile Cys Leu Asn Met Ile Thr Met Val 1485 1490 1495	4694
GAG ACC GAC GAG CAG GGC GAG GAG AAG ACG AAG GTT CTG GGC AGA ATC Glu Thr Asp Glu Gln Gly Glu Glu Lys Thr Lys Val Leu Gly Arg Ile 1500 1505 1510	4742
AAC CAG TTC TTT GTG GCC GTC TTC ACG GGC GAG TGT GTG ATG AAG ATG Asn Gln Phe Phe Val Ala Val Phe Thr Gly Glu Cys Val Met Lys Met 1515 1520 1525	4790
TTC GCC CTG CGA CAG TAC TAC TTC ACC AAC GGC TGG AAC GTG TTC GAC Phe Ala Leu Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp 1530 1535 1540 1545	4838
TTC ATA GTG GTG ATC CTG TCC ATT GGG AGT CTG CTG TTT TCT GCA ATC Phe Ile Val Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile 1550 1555 1560	4886
CTT AAG TCA CTG GAA AAC TAC TTC TCC CCG ACG CTC TTC CGG GTC ATC Leu Lys Ser Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile 1565 1570 1575	4934
CGT CTG GCC AGG ATC GGC CGC ATC CTC AGG CTG ATC CGA GCA GCC AAG Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys 1580 1585 1590	4982
GGG ATT CGC ACG CTG CTC TTC GCC CTC ATG ATG TCC CTG CCC GCC CTC Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu 1595 1600 1605	5030

92

TTC AAC ATC GGC CTC CTC CTC TTC CTC GTC ATG TTC ATC TAC TCC ATC Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile 1610 1615 1620 1625	5078
TTC GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC GGC ATC GAC Phe Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp 1630 1635 1640	5126
GAC ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG TGC CTG TTC Asp Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe 1645 1650 1655	5174
CAG ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC CCC ATC CTC Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu 1660 1665 1670	5222
AAC ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC AGC AAC GGC Asn Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly 1675 1680 1685	5270
TCC CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC TTC TTC ACC Ser Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr 1690 1695 1700 1705	5318
ACC TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATC GCA Thr Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala 1710 1715 1720	5366
GTG ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC ACG GAG CCC Val Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro 1725 1730 1735	5414
CTG AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG GAG AAG TTC Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe 1740 1745 1750	5462
GAC CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC TCA GAC TTC Asp Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe 1755 1760 1765	5510
GCG GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC AAC CAG AAT Ala Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn 1770 1775 1780 1785	5558
ATA TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT AAG ATC CAC Ile Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His 1790 1795 1800	5606
TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG GGA GAA TCC Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser 1805 1810 1815	5654
GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG TTT ATG GCG Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala 1820 1825 1830	5702
ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg 1835 1840 1845	5750
TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg 1850 1855 1860 1865	5798

93

AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG	5846
Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val	
1870 1875 1880	
CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC AGT	5894
Pro Arg Ala Glu Asp Gly Val Ser Leu Pro Gly Glu Tyr Ser	
1885 1890 1895	
ACA TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT	5942
Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser	
1900 1905 1910	
GCT ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT	5990
Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser	
1915 1920 1925	
GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG	6038
Asp Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu	
1930 1935 1940 1945	
GTC GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT	6084
Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln	
1950 1955	
CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG	6144
AGGTGGCACC AACCTCCAGC CTCCACCAAT GCATGTCACT GGTTCATGGTG TCAGAACTGA	6204
ATGGGGACAT CCTTGAGAAA GCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT	6264
CCATTCTGAC GTCCCTTCCG AGTTCCCAGA AGATGTCATT GCTCCCTTCT GTTTGTGACC	6324
AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG	6384
TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTGTTGTTACT GAGAATTAGG GTTTGCATGA	6444
CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTTA	6504
AAGTTAAAAA AAAAAAAAAA AAA	6527

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1957 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Glu	Leu	Pro	Phe	Ala	Ser	Val	Gly	Thr	Thr	Asn	Phe	Arg	Arg	Phe
1				5					10					15	
Thr	Pro	Glu	Ser	Leu	Ala	Glu	Ile	Glu	Lys	Gln	Ile	Ala	Ala	His	Arg
			20					25					30		
Ala	Ala	Lys	Lys	Ala	Arg	Thr	Lys	His	Arg	Gly	Gln	Glu	Asp	Lys	Gly
		35					40					45			
Glu	Lys	Pro	Arg	Pro	Gln	Leu	Asp	Leu	Lys	Asp	Cys	Asn	Gln	Leu	Pro
	50					55					60				

94

Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
 65 70 75 80
 Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
 85 90 95
 Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
 100 105 110
 Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
 115 120 125
 His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
 130 135 140
 Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
 145 150 155 160
 Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
 165 170 175
 Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
 180 185 190
 Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
 195 200 205
 Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
 210 215 220
 Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
 225 230 235 240
 His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
 245 250 255
 Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
 260 265 270
 Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
 275 280 285
 Leu Ser Ser Glu Met Ala Glu Tyr Ile Phe Ile Lys Pro Gly Thr Thr
 290 295 300
 Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320
 Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 325 330 335
 Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350
 Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
 355 360 365
 Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
 370 375 380
 Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
 385 390 395 400

95

Glu	Gln	Ser	Gln	Ala	Thr	Ile	Ala	Glu	Ile	Glu	Ala	Lys	Glu	Lys	Lys			
				405					410					415				
Phe	Gln	Glu	Ala	Leu	Glu	Val	Leu	Gln	Lys	Glu	Gln	Glu	Val	Leu	Ala			
			420					425					430					
Ala	Leu	Gly	Ile	Asp	Thr	Thr	Ser	Leu	Gln	Ser	His	Ser	Gly	Ser	Pro			
		435					440					445						
Leu	Ala	Ser	Lys	Asn	Ala	Asn	Glu	Arg	Arg	Pro	Arg	Val	Lys	Ser	Arg			
	450					455					460							
Val	Ser	Glu	Gly	Ser	Thr	Asp	Asp	Asn	Arg	Ser	Pro	Gln	Ser	Asp	Pro			
465					470					475					480			
Tyr	Asn	Gln	Arg	Arg	Met	Ser	Phe	Leu	Gly	Leu	Ser	Ser	Gly	Arg	Arg			
				485					490					495				
Arg	Ala	Ser	His	Gly	Ser	Val	Phe	His	Phe	Arg	Ala	Pro	Ser	Gln	Asp			
			500					505					510					
Ile	Ser	Phe	Pro	Asp	Gly	Ile	Thr	Pro	Asp	Asp	Gly	Val	Phe	His	Gly			
		515					520					525						
Asp	Gln	Glu	Ser	Arg	Arg	Gly	Ser	Ile	Leu	Leu	Gly	Arg	Gly	Ala	Gly			
	530					535					540							
Gln	Thr	Gly	Pro	Leu	Pro	Arg	Ser	Pro	Leu	Pro	Gln	Ser	Pro	Asn	Pro			
545					550					555					560			
Gly	Arg	Arg	His	Gly	Glu	Glu	Gly	Gln	Leu	Gly	Val	Pro	Thr	Gly	Glu			
				565					570					575				
Leu	Thr	Ala	Gly	Ala	Pro	Glu	Gly	Pro	Ala	Leu	Asp	Thr	Thr	Gly	Gln			
			580					585					590					
Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	Asn	Glu	Pro	Phe	Arg	Ala	Gln			
		595					600					605						
Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	Thr	Ser	Val	Ile	Glu	Glu	Leu			
	610					615					620							
Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	Cys	Leu	Ile	Ser	Phe	Ala	Gln			
625					630					635					640			
Lys	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	Lys	Trp	Arg	Lys	Phe	Lys	Met			
				645					650					655				
Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	Phe	Ala	Glu	Leu	Thr	Ile	Thr			
			660					665					670					
Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	Met	Ala	Met	Glu	His	Tyr	Pro			
		675					680					685						
Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	Gln	Ala	Gly	Asn	Ile	Val	Phe			
	690					695					700							
Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	Phe	Lys	Ile	Ile	Ala	Phe	Asp			
705					710					715					720			
Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	Asn	Ile	Phe	Asp	Cys	Val	Ile			
				725					730					735				

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Val Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu
 740 745 750
 Ser Val Leu Arg Ser Leu Arg Leu Leu Arg Val Phe Lys Leu Ala Lys
 755 760 765
 Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val
 770 775 780
 Gly Ala Leu Gly Asn Leu Thr Phe Ile Leu Ala Ile Ile Val Phe Ile
 785 790 795 800
 Phe Ala Leu Val Gly Lys Gln Leu Leu Ser Glu Asp Tyr Gly Cys Arg
 805 810 815
 Lys Asp Gly Val Ser Val Trp Asn Gly Glu Lys Leu Arg Trp His Met
 820 825 830
 Cys Asp Phe Phe His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly
 835 840 845
 Glu Trp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser
 850 855 860
 Ile Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val
 865 870 875 880
 Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Ala Asp
 885 890 895
 Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu
 900 905 910
 Ala Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ile
 915 920 925
 Ala Ser Tyr Ile Ser Ser His Cys Arg Phe Arg Trp Pro Lys Val Glu
 930 935 940
 Thr Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn
 945 950 955 960
 His Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys
 965 970 975
 Pro Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp
 980 985 990
 Pro Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu
 995 1000 1005
 Asp Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln
 1010 1015 1020
 Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys
 1025 1030 1035 1040
 Cys Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser
 1045 1050 1055
 Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser
 1060 1065 1070

97

Pro Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly
 1075 1080 1085
 Ser Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro
 1090 1095 1100
 Glu Leu Ala Asp Asp Leu Asp Glu Pro Asp Asp Cys Phe Thr Glu Gly
 1105 1110 1115 1120
 Cys Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro
 1125 1130 1135
 Trp Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu
 1140 1145 1150
 His Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser
 1155 1160 1165
 Gly Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val
 1170 1175 1180
 Lys Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val
 1185 1190 1195 1200
 Phe Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe
 1205 1210 1215
 Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu
 1220 1225 1230
 Thr Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile
 1235 1240 1245
 Lys Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser
 1250 1255 1260
 Arg Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile
 1265 1270 1275 1280
 Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile
 1285 1290 1295
 Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys
 1300 1305 1310
 Val Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val
 1315 1320 1325
 Asn Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe
 1330 1335 1340
 Trp Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu
 1345 1350 1355 1360
 Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr
 1365 1370 1375
 Ala Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn
 1380 1385 1390
 Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly
 1395 1400 1405

98

Phe Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn
 1410 1415 1420
 Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu
 1425 1430 1435 1440
 Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro
 1445 1450 1455
 Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe
 1460 1465 1470
 Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile
 1475 1480 1485
 Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu
 1490 1495 1500
 Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val
 1505 1510 1515 1520
 Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr
 1525 1530 1535
 Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser
 1540 1545 1550
 Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr
 1555 1560 1565
 Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg
 1570 1575 1580
 Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe
 1585 1590 1595 1600
 Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu
 1605 1610 1615
 Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala
 1620 1625 1630
 Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr
 1635 1640 1645
 Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly
 1650 1655 1660
 Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys
 1665 1670 1675 1680
 Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser
 1685 1690 1695
 Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe
 1700 1705 1710
 Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn
 1715 1720 1725
 Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp
 1730 1735 1740

99

Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe
 1745 1750 1755 1760

Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro
 1765 1770 1775

Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu
 1780 1785 1790

Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala
 1795 1800 1805

Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys
 1810 1815 1820

Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser
 1825 1830 1835 1840

Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser
 1845 1850 1855

Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser
 1860 1865 1870

Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly
 1875 1880 1885

Val Ser Leu Pro Gly Glu Gly Tyr Ser Thr Phe Met Ala Asn Ser Gly
 1890 1895 1900

Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser
 1905 1910 1915 1920

Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro
 1925 1930 1935

Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn
 1940 1945 1950

Ser Pro Gly Pro Gln
 1955

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCTTCGCT CAGAAGTATC T

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid

100

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCTCGCCGT TCCACACGGA GA

22

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Phe Arg Leu Met
1

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Gln Asp Phe Trp Glu Asn Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Gln Asp Tyr Trp Glu Asn Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids

101

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Gln Asp Cys Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gln Asp Ser Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Gln Asp Phe Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Gln Asp Ser Trp Glu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

102

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly	Ser	Thr	Asp	Asp	Asn	Arg	Ser	Pro	Gln	Ser	Asp	Pro	Tyr	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser	Pro	Lys	Glu	Asn	His	Gly	Asp	Phe	Ile
1				5					10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro	Asn	His	Asn	Gly	Ser	Arg	Gly	Asn
1				5				

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Arg	Leu	Leu	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

103

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTTGCTGCG GGTCTTCAAG C

21

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu	Arg	Ala	Leu	Pro	Leu	Arg	Ala	Leu	Ser	Arg	Phe	Glu	Gly
1				5					10				

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCGAGACAG AGCCCGCAGC G

21

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACGGGTGCCG CAAGGACGGC GTCTCCGTGT GGAACGGCGA GAAG

44

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid

104

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTATCCTT CCTCTTCCAG CTCTACCCA GGTATGGAGC CAGGT

45

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCCCGTACGC TGCAGCTCTT T

21

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCCGGGAAG GCTAC

15

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCGACACCA GAAAT

15

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid

105

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGATCCTCTA GAGTCGACCT GCAGAAGGAA

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGACGCAGGA CTCCTGGGAG CGCC

24

1060